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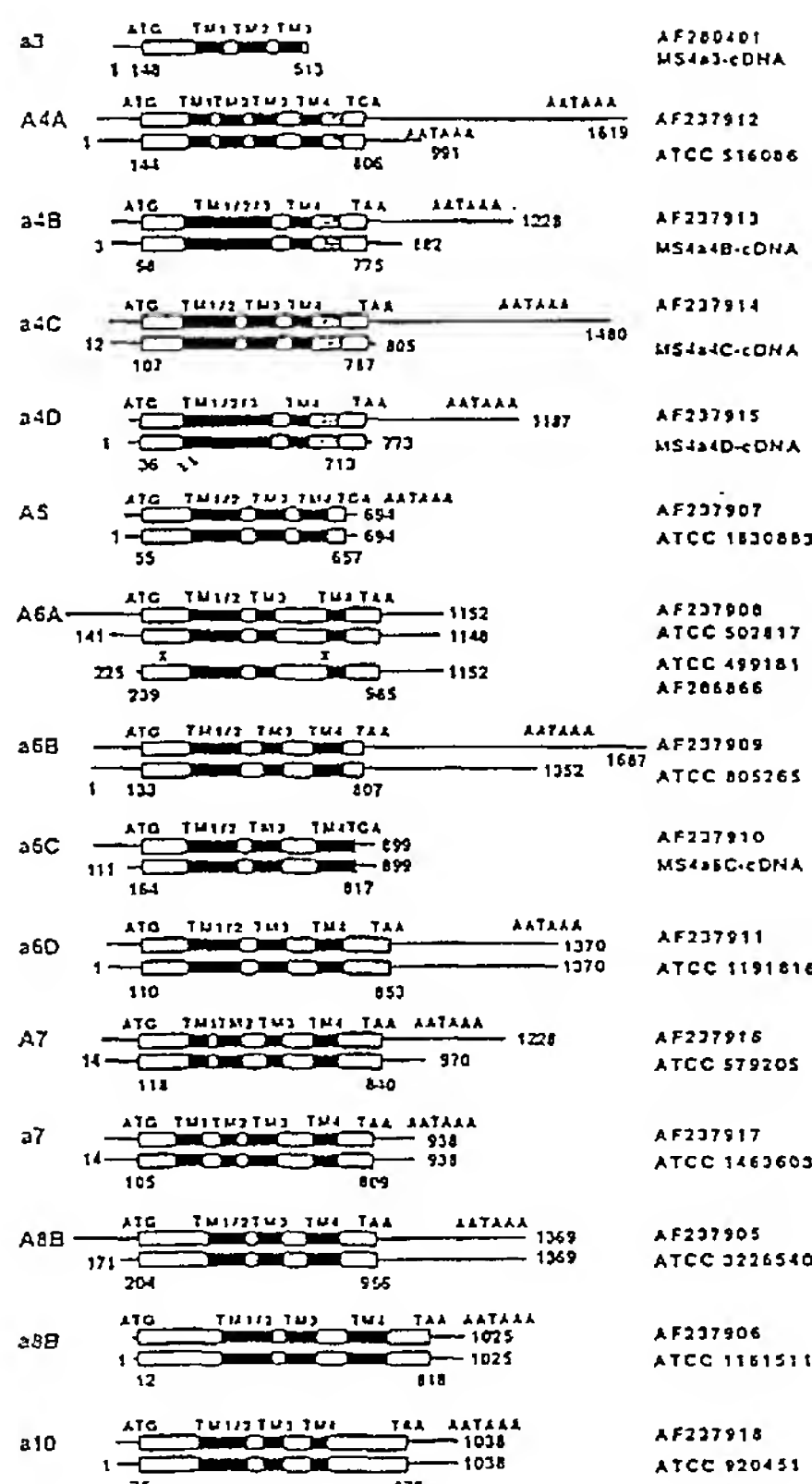
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(54) Title: IDENTIFICATION OF NOVEL MS4A GENE FAMILY MEMBERS EXPRESSED BY HEMATOPOIETIC CELLS



(57) Abstract: Isolated nucleic acids encoding MS4A polypeptides, isolated MS4A polypeptides, and uses thereof. The disclosed MS4A nucleic acids and polypeptides can be used to generate a mouse model of atopic disorders, for drug discovery screens, and for therapeutic treatment of atopic disorders or other MS4A-related conditions.



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DescriptionIDENTIFICATION OF NOVEL MS4A GENE FAMILY MEMBERS  
EXPRESSED BY HEMATOPOIETIC CELLS

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Cross Reference to Related Applications

This application is based on and claims priority to United States Provisional Application Serial Number 60/254,362, filed December 8, 2000, and United States Provisional Application Serial No. 60/270,057 filed February 20, 2001, herein incorporated by reference in their entirety.

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Grant Statement

This work was supported by NIH grants CA-81776 and CA-54464. Thus, the U.S. Government has rights in the invention.

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Field of the Invention

The present invention generally relates to a new class of MS4A proteins characterized by a membrane-embedded structure. More particularly, the present invention provides MS4A nucleic acid and polypeptide sequences, chimeric genes comprising disclosed MS4A sequences, antibodies that specifically recognize MS4A polypeptides, and uses thereof.

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Table of Abbreviations

	ATCC	American Tissue Culture Collection
25	CD20	CD20 B lymphocyte differentiation antigen
	FcεRIβ	high-affinity IgE receptor β chain
	GFP	green fluorescent protein
	htgs	GenBank human genomic database
	HTm4	hematopoietic CD20-like antigen
30	MS4A family	membrane spanning 4-domain family, subfamily A

### Background Art

CD20, Fc $\epsilon$ RI $\beta$ , and HTm4 are three cell surface proteins expressed by hematopoietic cells that represent members of a nascent gene family (Adra et al. (1999) *Clin Genet* 55:431-437, Kinet (1999) *Annu Rev Immunol* 17:931-972; Tedder and Engel (1994) *Immunol Today* 15:450-454). The deduced amino acid sequence of human and mouse CD20 first demonstrated a cell surface protein containing four membrane-spanning regions, N- and C-terminal cytoplasmic domains, and an ~50 amino acid loop that serves as the extracellular domain (Einfeld et al. (1988) *EMBO J* 7:711-717; Stamenkovic and Seed (1988) *J Exp Med* 167:1975-1980; Tedder et al. (1988a) *J Immunol* 141:4388-4394; Tedder et al. (1988b) *Proc Natl Acad Sci USA* 85:208-212). Human CD20 shares 20% amino acid sequence identity with Fc $\epsilon$ RI $\beta$  and HTm4 (Adra et al. (1994) *Proc Natl Acad Sci USA* 91:10178-10182, Küster et al. (1992) *J Biol Chem* 267:12782-12787). Moreover, these three proteins have a similar overall structure in man, mouse, and rat with significant sequence identity within the first three membrane-spanning domains (Kinet et al. (1988) *Proc Natl Acad Sci USA* 85:6483-6487; Ra et al. (1989) *Nature* 19:1771-7; Tedder et al., 1988a). In addition, all three genes are located in the same region of human chromosome 11q12-13.1 (Adra et al., 1994; Hupp et al. (1989) *J Immunol* 143:3787-3791; Tedder et al. (1989a) *J Immunol* 142:2555-2559) and mouse chromosome 19 (Hupp et al. 1989; Tedder et al., 1988a). These three genes are therefore likely to have evolved from a common precursor.

Despite structural and sequence conservation between CD20, Fc $\epsilon$ RI $\beta$  and HTm4, transcription of each gene is differentially regulated. CD20 is only expressed by B lymphocytes (Stashenko et al. (1980) *J Immunol* 125:1678-1685; Tedder et al., 1988a). Fc $\epsilon$ RI $\beta$  is expressed by mast cells and basophils (Kinet, 1999). HTm4 is expressed by diverse lymphoid and myeloid origin hematopoietic cells (Adra et al., 1994).

Although the function of HTm4 remains unexplored, CD20 and Fc $\epsilon$ RI $\beta$  have critical roles in cell signaling. CD20 forms a homo- or hetero-tetrameric complex that is functionally important for regulating cell cycle progression

and signal transduction in B lymphocytes (Tedder and Engel, 1994). CD20 additionally regulates transmembrane  $\text{Ca}^{++}$  conductance, possibly as a functional component of a  $\text{Ca}^{++}$ -permeable cation channel (Bubien et al. *J Cell Biol* 121:1121-1132; Kanzaki et al. (1997a) *J Biol Chem* 272:14733-14739; Kanzaki et al. (1997b) *J Biol Chem* 272:4964-4969; Kanzaki et al. (1995) *J Biol Chem* 270:13099-13104).  $\text{Fc}\epsilon\text{RI}\beta$  is part of a tetrameric receptor complex consisting of  $\alpha$ ,  $\beta$ , and two  $\gamma$  chains (Blank et al. (1989) *Nature* 337:187-189).  $\text{Fc}\epsilon\text{RI}\beta$  mediates interactions with IgE-bound antigens that lead to cellular responses such as the degranulation of mast cells. Specifically, the  $\text{Fc}\epsilon\text{RI}\beta$  subunit functions as an amplifier of  $\text{Fc}\epsilon\text{RI}\beta$ -mediated activation signals (Dombrowicz et al. (1998) *Immunity* 8:517-529; Lin et al. (1996) *Cell* 85:985-995). Because of their unique structure and sequence homology, CD20,  $\text{Fc}\epsilon\text{RI}\beta$ , and HTm4 are likely to share overlapping functional properties.

CD20 and  $\text{Fc}\epsilon\text{RI}\beta$  are also important clinically. Antibodies against CD20 are effective in treating non-Hodgkin's lymphoma (McLaughlin et al. (1998) *Oncology* 12:1763-1769; Onrust et al. (1989) *J Biol Chem* 264:15323-15327; Weiner (1999) *Semin Oncol* 26:43-51). Genetic variations at chromosome 11q12-13 can also play a role in the pathogenesis of allergic diseases (Adra et al., 1999; Kinet, 1999). Recent studies suggest that  $\text{Fc}\epsilon\text{RI}\beta$  contributes to such diseases, and other genetic elements in this region likely also contribute to allergic disease.

Since CD20,  $\text{Fc}\epsilon\text{RI}\beta$ , and HTm4 are likely to have evolved by duplication of an ancestral gene, other related proteins might exist that form additional receptor complexes. In view of the clinical importance noted above, the identification of such proteins thus represents a long-felt and ongoing need in the art. To address this need, applicants have identified novel human and mouse proteins that span the cell membrane at least four times and share high levels of amino acid sequence identity with CD20,  $\text{Fc}\epsilon\text{RI}\beta$ , and HTm4. This finding reveals a new gene family that has been designated herein as the MS4A family (membrane spanning 4-domain family, subfamily A). Currently this family contains at least 10 subgroups

(MS4A1 through MS4A12) that encode at least 21 previously unidentified human and mouse proteins expressed by hematopoietic cells and by diverse cell types in non-hematopoietic tissues.

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#### Summary of the Invention

The present invention discloses isolated MS4A polypeptides and isolated nucleic acid molecules encoding the same. Preferably, an isolated MS4A polypeptide, or functional portion thereof, comprises a polypeptide encoded by the nucleic acid molecule of any one of the odd numbered SEQ ID NOs:1-37 a polypeptide encoded by a nucleic acid molecule that is substantially identical to any one of the odd-numbered SEQ ID NOs:1-37, a polypeptide fragment encoded by a 20 nucleotide sequence that is identical to a contiguous 20 nucleotide sequence of any one of the odd-numbered SEQ ID NOs:1-37, a polypeptide having an amino acid sequence of any one of the even-numbered SEQ ID NOs:2-38, a polypeptide that is a biological equivalent of any one of the even-numbered SEQ ID NOs:2-38, or a polypeptide that is immunologically cross-reactive with an antibody that shows specific binding with a polypeptide comprising some or all amino acids of any one of the even-numbered SEQ ID NOs:2-38.

20 The present invention further teaches chimeric genes having a heterologous promoter that drives expression of a nucleic acid sequence encoding a MS4A polypeptide. Preferably, the chimeric gene is carried in a vector and introduced into a host cell so that a MS4A polypeptide of the present invention is produced. Preferred host cells include but are not limited to a bacterial cell, a hamster cell, a mouse cell, or a human cell.

25 In another aspect of the invention, a method is provided for detecting a nucleic acid molecule that encodes a MS4A polypeptide. According to the method, a biological sample having nucleic acid material is hybridized under stringent hybridization conditions to a MS4A nucleic acid molecule of the present invention. Such hybridization enables a nucleic acid molecule of the biological sample and the MS4A nucleic acid molecule to form a detectable duplex structure. Preferably, the MS4A nucleic acid molecule includes some

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or all nucleotides of any one of the odd-numbered SEQ ID NOs:1-37. Also preferably, the biological sample comprises human nucleic acid material.

The present invention further teaches an antibody that specifically recognizes a MS4A polypeptide. Preferably, the antibody recognizes some  
5 or all amino acids of any one of the even-numbered SEQ ID NOs:2-38. A method for producing a MS4A antibody is also disclosed, and the method comprises recombinantly or synthetically producing a MS4A polypeptide, or portion thereof; formulating the MS4A polypeptide so that it is an effective immunogen; immunizing an animal with the formulated polypeptide to  
10 generate an immune response that includes production of MS4A antibodies; and collecting blood serum from the immunized animal containing antibodies that specifically recognize a MS4A polypeptide. Antibody-producing cells can be optionally fused with an immortal cell line whereby a monoclonal antibody that specifically recognizes a MS4A polypeptide can be selected.  
15 Preferably, the MS4A polypeptide used as an immunogen includes some or all amino acid sequences of any one the even-numbered SEQ ID NOs:2-38.

A method is also provided for detecting a level of MS4A polypeptide using an antibody that specifically recognizes a MS4A polypeptide. According to the method, a biological sample is obtained from an  
20 experimental subject and a control subject, and a MS4A polypeptide is detected in the sample by immunochemical reaction with the MS4A antibody. Preferably, the antibody recognizes amino acids of any one of the even-numbered SEQ ID NOs:2-38, and is prepared according to a method of the present invention for producing such an antibody.

25 The present invention further discloses a method for identifying a compound that modulates MS4A function. The method comprises: exposing an isolated MS4A polypeptide to one or more compounds, and assaying binding of a compound to the isolated MS4A polypeptide. A compound is selected that demonstrates specific binding to the isolated MS4A  
30 polypeptide. Preferably, the MS4A polypeptide used in the binding assay of the method includes some or all amino acids of any one of the even-numbered SEQ ID NOs:2-38.



Also provided is a method for identifying a regulator of MS4A gene expression. The method comprises (a) exposing a cell sample with a candidate compound to be tested, the cell sample containing at least one cell containing a DNA construct comprising a modulatable transcriptional regulatory sequence of a MS4A-encoding nucleic acid and a reporter gene which is capable of producing a detectable signal; (b) evaluating an amount of signal produced in relation to a control sample; and (c) identifying a candidate compound as a modulator of MS4A gene expression based on the amount of signal produced in relation to a control sample. Preferably, the modulatable transcriptional regulatory sequence of a MS4A-encoding nucleic acid comprises a sequence that is immediately upstream of the initial coding region of a MS4A gene as set forth in any one of SEQ ID NOs:73-81.

The present invention further provides a method for modulating MS4A function in a subject. According to the method, a pharmaceutical composition is prepared that includes a substance capable of modulating MS4A expression or function, and a carrier. An effective dose of the pharmaceutical composition is administered to a subject, whereby MS4A activity is altered in the subject. Provided are therapeutic methods wherein a change in MS4A activity comprises a shift in the abundance of cell subpopulations expressing said protein, modulation of  $[Ca^{2+}]_i$  levels, or altered cell function. In a preferred embodiment, the substance used to perform this method shows specific binding to some or all amino acids of any one of the even-numbered SEQ ID NOs:2-38, and was discovered by a method of the present invention. In another embodiment, MS4A function is disrupted by immunizing a subject with an effective dose of the disclosed MS4A polypeptide. The immune system of the subject produces an antibody that specifically recognizes the MS4A polypeptide, and preferably recognizes some or all of amino acids of any one of the even-numbered SEQ ID NOs:2-38. In a further embodiment, a gene therapy vector is used, the vector comprising a nucleotide sequence encoding a MS4A polypeptide. Alternatively, the gene therapy vector comprises a nucleotide sequence encoding a nucleic acid molecule, a peptide, or a protein that interacts with a

MS4A nucleic acid or polypeptide. Preferably, the subject is a human subject.

Accordingly, it is an object of the present invention to provide novel MS4A nucleic acid and polypeptide sequences, and novel methods relating thereto. This object is achieved in whole or in part by the present invention.

An object of the invention having been stated above, other objects and advantages of the present invention will become apparent to those skilled in the art after a study of the following description of the invention, Figures and non-limiting Examples.

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#### Brief Description of the Drawings

Figure 1 depicts cDNAs encoded by fifteen new human or mouse MS4A gene products. Consensus sequences from cDNAs and overlapping ESTs are indicated by their GenBank Accession numbers. Representative full-length cDNAs for each gene product are shown, except for *MS4a3* which was not full-length. 5' and 3' untranslated sequences are shown as horizontal lines with relative nucleotide lengths shown. Coding regions are shown as boxes with translation initiation and termination codons and their relative nucleotide locations shown. Poly(A) attachment signal sequences (AATAAA) are indicated when known. Deduced hydrophobic regions are shown as filled boxes with the predicted membrane-spanning domains shown as TM1-TM4. Additional hydrophobic regions in MS4A4 proteins are shown as shaded boxes. Sites of putative nucleotide polymorphisms in *MS4A6A* are indicated by two (X)s.

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Figure 2 depicts exon-intron organization of the human MS4A genes. The maps were constructed by aligning known and predicted MS4A cDNA sequences with human genomic sequences as described in Materials and Methods. Exons are shown as boxes with the predicted translation initiation codons (ATG), transmembrane domains (TM) and termination codons indicated on the top. All exon and intron distances are shown to scale. Gaps indicate where intron distances have not been determined for *MS4A3*, *MS4A4A*, and *MS4A12*. Two long introns present in *MS4A4E* are not to

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scale but the intron lengths are indicated. Exon numbering for *MS4A1*, and *MS4A2* is as published (Küster et al., 1992; Tedder et al., 1988a; Tedder et al., 1988b).

Figure 3 shows human *MS4A4E* protein and transcript sequences  
5 predicted from genomic DNA sequences. *MS4A4E* sequences are  
compared with human *MS4A4A* cDNA (disclosed herein) and genomic  
sequences. Gaps were introduced to provide optimal alignment. The boxed  
AAC sequence near the 5' end of the *MS4A4A* sequence indicates the  
length of the most 5' *MS4A4A* cDNA sequence. Sequences upstream of this  
10 are based on contiguous genomic DNA sequences. Nucleotide numbering  
is based on the *MS4A4A* cDNA sequence, disclosed herein. Predicted  
translation initiation codons are shaded. Predicted membrane-spanning  
regions are underlined. An asterisk indicates predicted translation  
termination codons. Potential poly-A attachment signal sequences  
15 (AATAAA) are boxed.

Figure 4 shows human *MS4A6E* protein and transcript sequences  
predicted from genomic DNA and overlapping cDNA sequences.  
Predicted *MS4A6E* transcript sequences are compared with human *MS4A6A*  
cDNA sequence (disclosed herein). Gaps were introduced in the nucleotide  
20 sequence to provide optimal alignment. The 5' end of both transcripts start  
at 3' splice-acceptor sites which demark the first translated exons for both  
genes. The 5' end of the putative *MS4A6E* transcript is based on genomic  
DNA sequence, while the predicted sequences starting at nucleotide 60  
were based on both genomic DNA sequences and overlapping cDNA  
25 sequences. A gap in the *MS4A6A* sequence is indicated where TM1/2 and  
TM2 exons are not found in *MS4A6E* transcripts. *MS4A6A* nucleotide  
numbering is based on the cDNA sequence (disclosed herein). Predicted  
translation initiation codons are shaded. Predicted membrane-spanning  
regions are underlined. An asterisk indicates the predicted translation  
30 termination codon for the *MS4A6E* protein.

Figure 5 shows human *MS4A10* protein and transcript sequences  
predicted from human genomic DNA sequences. *MS4A10* nucleotide

sequence is compared with mouse *MS4a10* cDNA sequence (disclosed herein). The 5' end of both transcripts start at 3' splice-acceptor sites which demark the first translated exons for both genes. *MS4a10* nucleotide numbering is based on the cDNA sequence (disclosed herein). Predicted translation initiation codons are shaded. Predicted membrane-spanning regions are underlined. An asterisk indicates predicted translation termination codon for the MS4A10 protein. Potential poly-A attachment signal sequences (AATAAA) are boxed.

Figure 6 depicts a physical linkage map for the MS4A genes. A scheme for chromosome 11 structure is shown on the left with the mapped locations for *MS4A1*, *MS4A2* and *MS4A3* indicated. Representative human BAC clones are shown as vertical black bars with clone names shown on the top and clone size shown at the bottom. All distances are shown to the indicated scale. The distance between and spatial relationship of RP11-312N17 to the four other overlapping BACs shown at the bottom are unknown. Thin bars indicate continuous characterized (mapped or sequenced) regions of DNA that contain identified MS4A genes. When the relative position of this region of DNA is known relative to the representative BACs that are shown, the thin bars overlay the BAC. The mapped position of each MS4A gene is indicated on the right with the relative direction of gene translation indicated by arrows (  $\rightarrow$  ). In some cases, approximate distances between MS4A genes (termination codons to the translation initiation codon for the next gene) are indicated in base pairs (bp). In some cases, approximate MS4A gene size is indicated showing the distance between predicted translation initiation codons and translation termination codons as show in Figure 7.

Figure 7 depicts deduced amino acid sequences for CD20 (human A1, SEQ ID NO:40; mouse a1, SEQ ID NO:48), FcεRIβ (human A2, SEQ ID NO:42; mouse a2, SEQ ID NO:50), HTm4 (human A3, SEQ ID NO:44; mouse a3, SEQ ID NO:20), and 19 new MS4A (human) (even-numbered SEQ ID NOs:2-18, 46) and MS4a (mouse and pig) proteins (even-numbered SEQ ID NOs:22-38, 56). Gaps were introduced to optimize alignments.

Numbers represent predicted residue positions. The predicted membrane-spanning regions (TM1-TM4) are indicated. Predicted intron|exon splice junctions are indicated by vertical bars where information was available. Amino acids common to 10 or more proteins are shaded. \*indicates partial  
5 sequence for the MS4a3 protein. CD20, FcεRIβ, and HTm4 sequences and known intron|exon borders (SEQ ID NOs:39-44, 47-50) are as published (Adra et al., 1994; Küster et al., 1992; Ra et al., 1989; Tedder et al., 1988a; Tedder et al., 1989b; Tedder et al., 1988b). MS4A12 represents a conceptual translation (SEQ ID NO:46) of a human colon mucosa cDNA  
10 sequence (GenBank AK000224, SEQ ID NO:45), and MS4a12 represents a conceptual translation (SEQ ID NO:56) of a homologous cDNA sequence from pig (GenBank AJ236932, SEQ ID NO:55).

Figure 8 depicts UPGMA (unweighted pair group method using arithmetic averages) tree of deduced MS4A and MS4a protein sequences.  
15 Horizontal tree branch length is a measure of sequence relatedness. For example, MS4a4B and MS4a4C are the most similar in sequence, while CD20 (MS4A1) sequences were the most divergent from other family members. The MS4a12p sequence was from pig, while all other MS4a sequences were from mouse. The UPGMA tree was generated using  
20 Geneworks version 2.0 (IntelliGenetics, Inc., Mountain View, California, USA).

Figure 9 shows immunofluorescent detection of CD20 expression during B cell development. Single cell suspensions of leukocytes were isolated from wild-type mice, stained using MB20-13 (visualized using a PE-  
25 conjugated, anti-mouse IgG3 antibody) and anti-B220 (FITC-conjugated) monoclonal antibodies, and examined by two-color immunofluorescence staining with flow cytometry analysis. Quadrant gates indicate negative and positive populations of cells as determined using isotype-matched control monoclonal antibodies. The gated cell populations correspond to the cells  
30 described in Table 7, and are shown for reference. These results are representative of those obtained with six (6) two month-old wild type mice.

Figure 10 summarizes the strategy for targeted disruption of the mouse *CD20* gene.

Figure 10A shows genomic clones encoding *CD20*.

Figure 10B shows the intron-exon organization of the wild type *CD20* allele containing exons 5-8 (shaded squares).

Figure 10C shows the structure of the *CD20* targeting vector.

Figure 10D shows the predicted structure of the *CD20* allele after gene targeting in ES cells by homologous recombination. The *EcoR V* restriction site in exon 6 is deleted as indicated.

Figure 10E presents Southern blot analysis of tail DNA from two wild type and four *CD20*<sup>-/-</sup> mice. Genomic DNA was digested with *EcoR V*, transferred to nitrocellulose and hybridized with the 5' probe indicated in (D).

Figure 10F shows PCR amplification of genomic DNA from wild type and *CD20*<sup>-/-</sup> mice using primers that bind in exons 6 and 7. Amplification of glyceraldehyde-3-phosphate dehydrogenase (*G3PDH*) is shown as a positive control.

Figure 10G shows PCR amplification of cDNA generated from splenic RNA of wild type and *CD20*<sup>-/-</sup> mice. Each reaction mixture contained a sense primer that hybridized with sequences encoded by exon 3 and antisense primers that hybridized with either exon 6 or *Neo*<sup>r</sup> gene promoter sequences.

Figures 10H and 10I show reactivity of the MB20-13 monoclonal antibody with *CD20* cDNA-transfected (thick line) or untransfected (dashed line) 300.19 cells (Figure 10H) or Chinese Hamster Ovary (CHO) cells (Figure 10I). The thin lines represent *CD20* cDNA-transfected cells stained with secondary antibody alone or an isotype-control monoclonal antibody. Indirect immunofluorescence staining was visualized by flow cytometry analysis.

Figure 10J shows immunofluorescent staining of splenocytes from *CD20*<sup>-/-</sup> or wild type mice with MB20-13 (visualized using a PE-conjugated, anti-mouse IgG3 antibody) and anti-B220 (FITC-conjugated) monoclonal antibodies. Splenocytes from *CD20*<sup>-/-</sup> mice generated histograms identical to

those obtained without MB20-1 monoclonal antibody present, using the secondary antibody alone.

Figure 11 depicts immunofluorescent detection of B lymphocyte subpopulations in CD20<sup>-/-</sup> and wild type mice. Lymphocytes were isolated and examined by two color immunofluorescent staining with flow cytometry analysis. Quadrants delineated by squares indicate negative and positive populations of cells as determined using unreactive monoclonal antibody controls. The gated cell populations correspond to the cells described in Table 7 that represent at least 6 mice of each genotype.

Figure 12 shows altered signal transduction in CD20<sup>-/-</sup> B cells. Figure 12 also shows CD19 expression by splenocytes from CD20<sup>-/-</sup> (thin line) and wild type (thick line) mice. Immunofluorescence staining using PE-conjugated anti-CD19 monoclonal antibody with flow cytometry analysis. The dashed line represents staining of wild type splenocytes with a control antibody.

Figure 12A presents calcium responses induced by BCR or CD19 ligation in CD20<sup>-/-</sup> and wild type B cells. Splenocytes were loaded with 1  $\mu$ M indo-1-AM ester and B cells were stained with FITC-conjugated anti-B220 antibody. At 1 min (arrow), optimal concentrations of goat anti-IgM F(ab')<sub>2</sub> antibody fragments, anti-CD19 monoclonal antibody or Thapsigargin were added, with or without EGTA present. Increased ratios of indo-1 fluorescence indicate increased [Ca<sup>2+</sup>]<sub>i</sub>. Results represent those from at least four experiments.

Figure 12B presents assays of tyrosine phosphorylation of proteins from purified splenic B cells of CD20<sup>-/-</sup> and wild type mice. B cells (2 x 10<sup>7</sup>/sample) were incubated with anti-IgM antibody for the times shown and detergent lysed. Proteins were resolved by SDS-PAGE, transferred to nitrocellulose and immunoblotted with anti-phosphotyrosine (anti-PTyr) antibody. The blot was stripped and reprobed with anti-SHP-1 antibody as a control for equivalent protein loading. Western blots from two of three experiments are shown to demonstrate the range of results.



### Detailed Description of the Invention

The present invention provides isolated nucleic acids encoding MS4A polypeptides (representative embodiments set forth as the odd-numbered SEQ ID NOs:1-37), isolated MS4A polypeptides (representative  
5 embodiments set forth as the even-numbered SEQ ID NOs:2-38), and uses thereof. The disclosed MS4A nucleic acids and polypeptides can be used according to methods of the present invention for drug discovery screens, for therapeutic treatment of atopic conditions, and for therapeutic regulation of  $[Ca^{2+}]_i$  levels, among other uses.

#### I. DEFINITIONS

While the following terms are believed to be well understood by one of ordinary skill in the art, the following definitions are set forth to facilitate explanation of the invention. The entire contents of all publications  
15 mentioned herein, including the discussion of the background art presented above, are hereby fully incorporated by reference.

##### I.A. MS4A nucleic acids

The nucleic acid molecules provided by the present invention include the isolated nucleic acid molecules of any one of the odd-numbered SEQ ID  
20 NOs:1-37, sequences substantially similar to sequences of any one of the odd-numbered SEQ ID NOs:1-37, conservative variants thereof, subsequences and elongated sequences thereof, complementary DNA molecules, and corresponding RNA molecules. The present invention also encompasses genes, cDNAs, chimeric genes, and vectors comprising  
25 disclosed MS4A nucleic acid sequences.

The term "nucleic acid molecule" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides which have similar  
30 properties as the reference natural nucleic acid. Unless otherwise indicated, a particular nucleotide sequence also implicitly encompasses conservatively modified variants thereof (e.g. degenerate codon substitutions),

complementary sequences, subsequences, elongated sequences, as well as the sequence explicitly indicated. The terms "nucleic acid molecule" or "nucleotide sequence" can also be used in place of "gene", "cDNA", or "mRNA". Nucleic acids can be derived from any source, including any  
5 organism.

The term "isolated", as used in the context of a nucleic acid molecule, indicates that the nucleic acid molecule exists apart from its native environment and is not a product of nature. An isolated DNA molecule can exist in a purified form or can exist in a non-native environment such as a  
10 transgenic host cell.

The term "purified", when applied to a nucleic acid, denotes that the nucleic acid is essentially free of other cellular components with which it is associated in the natural state. Preferably, a purified nucleic acid molecule is a homogeneous dry or aqueous solution. The term "purified" denotes that  
15 a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid is at least about 50% pure, more preferably at least about 85% pure, and most preferably at least about 99% pure.

The term "substantially identical", in the context of two nucleotide or  
20 amino acid sequences, can also be defined as two or more sequences or subsequences that have at least 60%, preferably 80%, more preferably 90-95%, and most preferably at least 99% nucleotide or amino acid sequence identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms  
25 (described herein below under the heading Nucleotide and Amino Acid Sequence Comparisons) or by visual inspection. Preferably, the substantial identity exists in nucleotide sequences of at least 50 residues, more preferably in nucleotide sequence of at least about 100 residues, more preferably in nucleotide sequences of at least about 150 residues, and most  
30 preferably in nucleotide sequences comprising complete coding sequences. In one aspect, polymorphic sequences can be substantially identical sequences. The term "polymorphic" refers to the occurrence of two or more



genetically determined alternative sequences or alleles in a population. An allelic difference can be as small as one base pair.

Another indication that two nucleotide sequences are substantially identical is that the two molecules specifically or substantially hybridize to each other under stringent conditions. In the context of nucleic acid hybridization, two nucleic acid sequences being compared can be designated a "probe" and a "target". A "probe" is a reference nucleic acid molecule, and a "target" is a test nucleic acid molecule, often found within a heterogenous population of nucleic acid molecules. A "target sequence" is synonymous with a "test sequence".

A preferred nucleotide sequence employed for hybridization studies or assays includes probe sequences that are complementary to or mimic at least an about 14 to 40 nucleotide sequence of a nucleic acid molecule of the present invention. Preferably, probes comprise 14 to 20 nucleotides, or even longer where desired, such as 30, 40, 50, 60, 100, 200, 300, or 500 nucleotides or up to the full length of any of those set forth as the odd-numbered SEQ ID NOs:1-37. Such fragments can be readily prepared by, for example, directly synthesizing the fragment by chemical synthesis, by application of nucleic acid amplification technology, or by introducing selected sequences into recombinant vectors for recombinant production.

The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex nucleic acid mixture (e.g., total cellular DNA or RNA). The phrase "binds substantially to" refers to complementary hybridization between a probe nucleic acid molecule and a target nucleic acid molecule and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired hybridization.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern blot analysis are both sequence- and environment-dependent. Longer sequences hybridize specifically at higher temperatures.

An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes, part I chapter 2, Elsevier, New York, New York. Generally, highly stringent hybridization and wash conditions are  
5 selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. Typically, under "stringent conditions" a probe will hybridize specifically to its target subsequence, but to no other sequences.

The  $T_m$  is the temperature (under defined ionic strength and pH) at  
10 which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the  $T_m$  for a particular probe. An example of stringent hybridization conditions for Southern or Northern Blot analysis of complementary nucleic acids having more than about 100 complementary residues is overnight hybridization in 50%  
15 formamide with 1 mg of heparin at 42°C. An example of highly stringent wash conditions is 15 minutes in 0.1 5 M NaCl at 65°C. An example of stringent wash conditions is 15 minutes in 0.2X SSC buffer at 65°C (See Sambrook et al. eds. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York for a  
20 description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example of medium stringency wash conditions for a duplex of more than about 100 nucleotides, is 15 minutes in 1X SSC at 45°C. An example of low stringency wash for a duplex of more than about 100 nucleotides, is 15 minutes in 4-6X  
25 SSC at 40°C. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.0 M  $\text{Na}^+$  ion, typically about 0.01 to 1.0 M  $\text{Na}^+$  ion concentration (or other salts) at pH 7.0-8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents  
30 such as formamide. In general, a signal to noise ratio of 2-fold (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization.

The following are examples of hybridization and wash conditions that can be used to clone homologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a probe nucleotide sequence preferably hybridizes to a target  
5 nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C followed by washing in 2X SSC, 0.1% SDS at 50°C; more preferably, a probe and target sequence hybridize in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C followed by washing in 1X SSC, 0.1% SDS at 50°C; more preferably, a probe and target sequence  
10 hybridize in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C followed by washing in 0.5X SSC, 0.1% SDS at 50°C; more preferably, a probe and target sequence hybridize in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C followed by washing in 0.1X SSC, 0.1% SDS at 50°C; more preferably, a probe and target sequence hybridize in 7%  
15 sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C followed by washing in 0.1X SSC, 0.1% SDS at 65°C.

A further indication that two nucleic acid sequences are substantially identical is that proteins encoded by the nucleic acids are substantially identical, share an overall three-dimensional structure, are biologically  
20 functional equivalents, or are immunologically cross-reactive. These terms are defined further under the heading MS4A Polypeptides herein below. Nucleic acid molecules that do not hybridize to each other under stringent conditions are still substantially identical if the corresponding proteins are substantially identical. This can occur, for example, when two nucleotide  
25 sequences are significantly degenerate as permitted by the genetic code.

The term "conservatively substituted variants" refers to nucleic acid sequences having degenerate codon substitutions wherein the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al. (1991) *Nucleic Acids Res* 19:5081;  
30 Ohtsuka et al. (1985) *J Biol Chem* 260:2605-2608; Rossolini et al. (1994) *Mol Cell Probes* 8:91-98).

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer nucleic acid sequence. An exemplary subsequence is a probe, described herein above, or a primer. The term "primer" as used herein refers to a contiguous sequence comprising about 8  
5 or more deoxyribonucleotides or ribonucleotides, preferably 10-20 nucleotides, and more preferably 20-30 nucleotides of a selected nucleic acid molecule. The primers of the invention encompass oligonucleotides of sufficient length and appropriate sequence so as to provide initiation of polymerization on a nucleic acid molecule of the present invention.

10 The term "elongated sequence" refers to an addition of nucleotides (or other analogous molecules) incorporated into the nucleic acid. For example, a polymerase (e.g., a DNA polymerase), e.g., a polymerase which adds sequences at the 3' terminus of the nucleic acid molecule. In addition, the nucleotide sequence can be combined with other DNA sequences, such  
15 as promoters, promoter regions, enhancers, polyadenylation signals, intronic sequences, additional restriction enzyme sites, multiple cloning sites, and other coding segments.

The term "complementary sequence", as used herein, indicates two nucleotide sequences that comprise antiparallel nucleotide sequences  
20 capable of pairing with one another upon formation of hydrogen bonds between base pairs. As used herein, the term "complementary sequences" means nucleotide sequences which are substantially complementary, as can be assessed by the same nucleotide comparison set forth above, or is defined as being capable of hybridizing to the nucleic acid segment in  
25 question under relatively stringent conditions such as those described herein. A particular example of a complementary nucleic acid segment is an antisense oligonucleotide.

The term "gene" refers broadly to any segment of DNA associated with a biological function. A gene encompasses sequences including but not  
30 limited to a coding sequence, a promoter region, a cis-regulatory sequence, a non-expressed DNA segment is a specific recognition sequence for regulatory proteins, a non-expressed DNA segment that contributes to gene

expression, a DNA segment designed to have desired parameters, or combinations thereof. A gene can be obtained by a variety of methods, including cloning from a biological sample, synthesis based on known or predicted sequence information, and recombinant derivation of an existing  
5 sequence.

The term "gene expression" generally refers to the cellular processes by which a biologically active polypeptide is produced from a DNA sequence.

The present invention also encompasses chimeric genes comprising  
10 the disclosed MS4A sequences. The term "chimeric gene", as used herein, refers to a promoter region operably linked to a MS4A coding sequence, a nucleotide sequence producing an antisense RNA molecule, a RNA molecule having tertiary structure, such as a hairpin structure, or a double-stranded RNA molecule.

15 The term "operably linked", as used herein, refers to a promoter region that is connected to a nucleotide sequence in such a way that the transcription of that nucleotide sequence is controlled and regulated by that promoter region. Techniques for operatively linking a promoter region to a nucleotide sequence are well known in the art.

20 The terms "heterologous gene", "heterologous DNA sequence", "heterologous nucleotide sequence", "exogenous nucleic acid molecule", or "exogenous DNA segment", as used herein, each refer to a sequence that originates from a source foreign to an intended host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a  
25 host cell includes a gene that is endogenous to the particular host cell but has been modified, for example by mutagenesis or by isolation from native cis-regulatory sequences. The terms also include non-naturally occurring multiple copies of a naturally occurring nucleotide sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or  
30 homologous to the cell but in a position within the host cell nucleic acid wherein the element is not ordinarily found.

The term "promoter region" defines a nucleotide sequence within a



gene that is positioned 5' to a coding sequence of a same gene and functions to direct transcription of the coding sequence. The promoter region includes a transcriptional start site and at least one cis-regulatory element. The present invention encompasses nucleic acid sequences that  
5 comprise a promoter region of a MS4A gene, or functional portion thereof.

The term "cis-acting regulatory sequence" or "cis-regulatory motif" or "response element", as used herein, each refer to a nucleotide sequence that enables responsiveness to a regulatory transcription factor. Responsiveness can encompass a decrease or an increase in  
10 transcriptional output and is mediated by binding of the transcription factor to the DNA molecule comprising the response element.

The term "transcription factor" generally refers to a protein that modulates gene expression by interaction with the cis-regulatory element and cellular components for transcription, including RNA Polymerase, Transcription Associated Factors (TAFs), chromatin-remodeling proteins,  
15 and any other relevant protein that impacts gene transcription.

A "functional portion" of a promoter gene fragment is a nucleotide sequence within a promoter region that is required for normal gene transcription. To determine nucleotide sequences that are functional, the  
20 expression of a reporter gene is assayed when variably placed under the direction of a promoter region fragment.

Promoter region fragments can be conveniently made by enzymatic digestion of a larger fragment using restriction endonucleases or DNase I. Preferably, a functional promoter region fragment comprises about 5000  
25 nucleotides, more preferably 2000 nucleotides, more preferably about 1000 nucleotides. Even more preferably a functional promoter region fragment comprises about 500 nucleotides, even more preferably a functional promoter region fragment comprises about 100 nucleotides, and even more preferably a functional promoter region fragment comprises about 20  
30 nucleotides.

The terms "reporter gene" or "marker gene" or "selectable marker" each refer to a heterologous gene encoding a product that is readily

observed and/or quantitated. A reporter gene is heterologous in that it originates from a source foreign to an intended host cell or, if from the same source, is modified from its original form. Non-limiting examples of detectable reporter genes that can be operably linked to a transcriptional regulatory region can be found in Alam & Cook (1990) *Anal Biochem* 188:245-254 and PCT International Publication No. WO 97/47763. Preferred reporter genes for transcriptional analyses include the *lacZ* gene (See, e.g., Rose & Botstein (1983) *Meth Enzymol* 101:167-180), Green Fluorescent Protein (GFP) (Cubitt et al. (1995) *Trends Biochem Sci* 20:448-455), luciferase, or chloramphenicol acetyl transferase (CAT). Preferred reporter genes for methods to produce transgenic animals include but are not limited to antibiotic resistance genes, and more preferably the antibiotic resistance gene confers neomycin resistance. Any suitable reporter and detection method can be used, and it will be appreciated by one of skill in the art that no particular choice is essential to or a limitation of the present invention.

An amount of reporter gene can be assayed by any method for qualitatively or preferably, quantitatively determining presence or activity of the reporter gene product. The amount of reporter gene expression directed by each test promoter region fragment is compared to an amount of reporter gene expression to a control construct comprising the reporter gene in the absence of a promoter region fragment. A promoter region fragment is identified as having promoter activity when there is significant increase in an amount of reporter gene expression in a test construct as compared to a control construct. The term "significant increase", as used herein, refers to an quantified change in a measurable quality that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater relative to a control measurement, more preferably an increase by about 5-fold or greater, and most preferably an increase by about 10-fold or greater.

The present invention further includes vectors comprising the disclosed MS4A sequences, including plasmids, cosmids, and viral vectors.



The term "vector", as used herein refers to a DNA molecule having sequences that enable its replication in a compatible host cell. A vector also includes nucleotide sequences to permit ligation of nucleotide sequences within the vector, wherein such nucleotide sequences are also replicated in a compatible host cell. A vector can also mediate recombinant production of a MS4A polypeptide, as described further herein below. Preferred vectors include but are not limited to pBluescript (Stratagene), pUC18, pBLCAT3 (Luckow & Schutz (1987) *Nucleic Acids Res* 15:5490), pLNTK (Gorman et al. (1996) *Immunity* 5:241-252), and pBAD/gIII (Stratagene). A preferred host cell is a mammalian cell; more preferably the cell is a Chinese hamster ovary cell, a HeLa cell, a baby hamster kidney cell, or a mouse cell; even more preferably the cell is a human cell.

Nucleic acids of the present invention can be cloned, synthesized, recombinantly altered, mutagenized, or combinations thereof. Standard recombinant DNA and molecular cloning techniques used to isolate nucleic acids are well known in the art. Exemplary, non-limiting methods are described by Sambrook et al., eds. (1989); by Silhavy et al. (1984) Experiments with Gene Fusions, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; by Ausubel et al. (1992) Current Protocols in Molecular Biology, John Wiley and Sons, Inc., New York, New York; and by Glover, ed. (1985) DNA Cloning: A Practical Approach, MRL Press, Ltd., Oxford, United Kingdom. Site-specific mutagenesis to create base pair changes, deletions, or small insertions are also well known in the art as exemplified by publications, see, e.g., Adelman et al., (1983) *DNA* 2:183; Sambrook et al. (1989).

Sequences detected by methods of the invention can be detected, subcloned, sequenced, and further evaluated by any measure well known in the art using any method usually applied to the detection of a specific DNA sequence including but not limited to dideoxy sequencing, PCR, oligomer restriction (Saiki et al. (1985) *Bio/Technology* 3:1008-1012), allele-specific oligonucleotide (ASO) probe analysis (Conner et al. (1983) *Proc Natl Acad Sci USA* 80:278), and oligonucleotide ligation assays (OLAs) (Landgren et.

al. (1988) *Science* 241:1007). Molecular techniques for DNA analysis have been reviewed (Landgren et. al. (1988) *Science* 242:229-237).

#### I.B. MS4A Polypeptides

The polypeptides provided by the present invention include the  
5 isolated polypeptides set forth as the even-numbered SEQ ID NOs:2-38, polypeptides substantially similar to the even-numbered SEQ ID NOs:2-38, MS4A polypeptide fragments, fusion proteins comprising MS4A amino acid sequences, biologically functional analogs, and polypeptides that cross-react with an antibody that specifically recognizes a MS4A polypeptide.

10 The term "isolated", as used in the context of a polypeptide, indicates that the polypeptide exists apart from its native environment and is not a product of nature. An isolated polypeptide can exist in a purified form or can exist in a non-native environment such as, for example, in a transgenic host cell.

15 The term "purified", when applied to a polypeptide, denotes that the polypeptide is essentially free of other cellular components with which it is associated in the natural state. Preferably, a polypeptide is a homogeneous solid or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel  
20 electrophoresis or high performance liquid chromatography. A polypeptide which is the predominant species present in a preparation is substantially purified. The term "purified" denotes that a polypeptide gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the polypeptide is at least about 50% pure, more preferably at least about 85%  
25 pure, and most preferably at least about 99% pure.

The term "substantially identical" in the context of two or more polypeptides sequences is measured by (a) polypeptide sequences having about 35%, or 45%, or preferably from 45-55%, or more preferably 55-65%, or most preferably 65% or greater amino acids which are identical or  
30 functionally equivalent. Percent "identity" and methods for determining identity are defined herein below under the heading Nucleotide and Amino Acid Sequence Comparisons.

Substantially identical polypeptides also encompass two or more polypeptides sharing a conserved three-dimensional structure. Computational methods can be used to compare structural representations, and structural models can be generated and easily tuned to identify similarities around important active sites or ligand binding sites. See 5 Henikoff et al. (2000) *Electrophoresis* 21(9):1700-1706; Huang et al. (2000) *Pac Symp Biocomput* 230-241; Saqi et al. (1999) *Bioinformatics* 15(6):521-522; and Barton (1998) *Acta Crystallogr D Biol Crystallogr* 54:1139-1146.

The term "functionally equivalent" in the context of amino acid 10 sequences is well known in the art and is based on the relative similarity of the amino acid side-chain substituents. See Henikoff & Henikoff (2000) *Adv Protein Chem* 54:73-97. Relevant factors for consideration include side-chain hydrophobicity, hydrophilicity, charge, and size. For example, arginine, lysine, and histidine are all positively charged residues; that 15 alanine, glycine, and serine are all of similar size; and that phenylalanine, tryptophan, and tyrosine all have a generally similar shape. By this analysis, described further herein below, arginine, lysine, and histidine; alanine, glycine, and serine; and phenylalanine, tryptophan, and tyrosine; are defined herein as biologically functional equivalents.

20 In making biologically functional equivalent amino acid substitutions, the hydropathic index of amino acids can be considered. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics, these are: isoleucine (+ 4.5); valine (+ 4.2); leucine (+ 3.8); phenylalanine (+ 2.8); cysteine (+ 2.5); methionine (+ 1.9); 25 alanine (+ 1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

The importance of the hydropathic amino acid index in conferring 30 interactive biological function on a protein is generally understood in the art (Kyte et al. (1982) *J Mol Biol* 157:105.). It is known that certain amino acids can be substituted for other amino acids having a similar hydropathic index

or score and still retain a similar biological activity. In making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within  $\pm 2$  of the original value is preferred, those which are within  $\pm 1$  of the original value are particularly preferred, and those  
5 within  $\pm 0.5$  of the original value are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent No. 4,554,101 states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with  
10 its immunogenicity and antigenicity, *i.e.* with a biological property of the protein. It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent protein.

As detailed in U.S. Patent No. 4,554,101, the following hydrophilicity  
15 values have been assigned to amino acid residues: arginine (+ 3.0); lysine (+ 3.0); aspartate (+ 3.0 $\pm$ 1); glutamate (+ 3.0 $\pm$ 1); serine (+ 0.3); asparagine (+ 0.2); glutamine (+ 0.2); glycine (0); threonine (-0.4); proline (-0.5 $\pm$ 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5);  
20 tryptophan (-3.4) .

In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within  $\pm 2$  of the original value is preferred, those which are within  $\pm 1$  of the original value are particularly preferred, and those within  $\pm 0.5$  of the original value are even  
25 more particularly preferred.

The present invention also encompasses MS4A polypeptide fragments or functional portions of a MS4A polypeptide. Such functional portion need not comprise all or substantially all of the amino acid sequence of a native MS4A gene product. The term "functional" includes any  
30 biological activity or feature of MS4A, including immunogenicity.

The present invention also includes longer sequences of a MS4A polypeptide, or portion thereof. For example, one or more amino acids can

be added to the N-terminus or C-terminus of a MS4A polypeptide. Fusion proteins comprising MS4A polypeptide sequences are also provided within the scope of the present invention. Methods of preparing such proteins are known in the art.

5           The present invention also encompasses functional analogs of a MS4A polypeptide. Functional analogs share at least one biological function with a MS4A polypeptide. An exemplary function is immunogenicity. In the context of amino acid sequence, biologically functional analogs, as used  
10           can be substituted. Functional analogs can be created at the level of the corresponding nucleic acid molecule, altering such sequence to encode desired amino acid changes. In one embodiment, changes can be introduced to improve the antigenicity of the protein. In another embodiment, a MS4A polypeptide sequence is varied so as to assess the  
15           activity of a mutant MS4A polypeptide.

          The present invention also encompasses recombinant production of the disclosed MS4A polypeptides. Briefly, a nucleic acid sequence encoding a MS4A polypeptide, or portion thereof, is cloned into a expression cassette, the cassette is introduced into a host organism, where it is recombinantly  
20           produced.

          The term "expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of interest which is operably linked to termination  
25           signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The expression cassette comprising the nucleotide sequence of interest can be chimeric. The expression cassette can also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression.

30           The expression of the nucleotide sequence in the expression cassette can be under the control of a constitutive promoter or an inducible promoter which initiates transcription only when the host cell is exposed to some



particular external stimulus. Exemplary promoters include Simian virus 40  
early promoter, a long terminal repeat promoter from retrovirus, an action  
promoter, a heat shock promoter, and a metallothien protein. In the case of  
a multicellular organism, the promoter and promoter region can direct  
5 expression to a particular tissue or organ or stage of development.  
Exemplary tissue-specific promoter regions include a MS4A promoter,  
described herein. Suitable expression vectors which can be used include,  
but are not limited to, the following vectors or their derivatives: human or  
animal viruses such as vaccinia virus or adenovirus, yeast vectors,  
10 bacteriophage vectors (e.g., lambda phage), and plasmid and cosmids DNA  
vectors.

The term "host cell", as used herein, refers to a cell into which a  
heterologous nucleic acid molecule has been introduced. Transformed cells,  
tissues, or organisms are understood to encompass not only the end product  
15 of a transformation process, but also transgenic progeny thereof.

A host cell strain can be chosen which modulates the expression of  
the inserted sequences, or modifies and processes the gene product in the  
specific fashion desired. For example, different host cells have  
characteristic and specific mechanisms for the translational and post-  
20 transactional processing and modification (e.g., glycosylation,  
phosphorylation of proteins). Appropriate cell lines or host systems can be  
chosen to ensure the desired modification and processing of the foreign  
protein expressed. Expression in a bacterial system can be used to produce  
a non-glycosylated core protein product. Expression in yeast will produce a  
25 glycosylated product. Expression in animal cells can be used to ensure  
"native" glycosylation of a heterologous protein.

Expression constructs are transfected into a host cell by any standard  
method, including electroporation, calcium phosphate precipitation, DEAE-  
Dextran transfection, liposome-mediated transfection, and infection using a  
30 retrovirus. The MS4A-encoding nucleotide sequence carried in the  
expression construct can be stably integrated into the genome of the host or  
it can be present as an extrachromosomal molecule.

Isolated polypeptides and recombinantly produced polypeptides can be purified and characterized using a variety of standard techniques that are well known to the skilled artisan. See, e.g. Ausubel et al. (1992), Bodanszky, et al. (1976) Peptide Synthesis, John Wiley and Sons, Second Edition, New York, New York and Zimmer et al. (1993) Peptides, pp. 393–394, ESCOM Science Publishers, B. V.

#### I.C. Nucleotide and Amino Acid Sequence Comparisons

The terms "identical" or percent "identity" in the context of two or more nucleotide or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms disclosed herein or by visual inspection.

The term "substantially identical" in regards to a nucleotide or polypeptide sequence means that a particular sequence varies from the sequence of a naturally occurring sequence by one or more deletions, substitutions, or additions, the net effect of which is to retain at least some of biological activity of the natural gene, gene product, or sequence. Such sequences include "mutant" sequences, or sequences wherein the biological activity is altered to some degree but retains at least some of the original biological activity. The term "naturally occurring", as used herein, is used to describe a composition that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism, which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer program, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are selected. The sequence comparison algorithm then calculates the percent sequence



identity for the designated test sequence(s) relative to the reference sequence, based on the selected program parameters.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman (1981) *Adv Appl Math* 2:482, by the homology alignment algorithm of Needleman & Wunsch (1970) *J Mol Biol* 48:443, by the search for similarity method of Pearson & Lipman (1988) *Proc Natl Acad Sci USA* 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, Madison, WI), or by visual inspection. See generally, Ausubel et al., 1992.

A preferred algorithm for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. (1990) *J Mol Biol* 215: 403-410. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the

alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength  $W=11$ , an expectation  $E=10$ , a cutoff of 100,  $M=5$ ,  $N=-4$ , and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength ( $W$ ) of 3, an expectation ( $E$ ) of 10, and the BLOSUM62 scoring matrix. See Henikoff & Henikoff (1989) *Proc Natl Acad Sci USA* 89:10915.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) *Proc Natl Acad Sci USA* 90:5873-5887. One measure of similarity provided by the BLAST algorithm is the smallest sum probability ( $P(N)$ ), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

#### I.D. Antibodies

The present invention also provides an antibody that specifically binds a MS4A polypeptide. The term "antibody" indicates an immunoglobulin protein, or functional portion thereof, including a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single chain antibody, Fab fragments, and an Fab expression library. "Functional portion" refers to the part of the protein that binds a molecule of interest. In a preferred embodiment, an antibody of the invention is a monoclonal antibody. Techniques for preparing and characterizing antibodies are well known in the art (See, e.g., Harlow & Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). A monoclonal antibody of the present invention can be readily prepared through use of well-known techniques such as the hybridoma techniques exemplified in U.S. Patent No 4,196,265 and the phage-displayed techniques disclosed in U.S. Patent No. 5,260,203.

The phrase "specifically (or selectively) binds to an antibody", or "specifically (or selectively) immunoreactive with", when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in a heterogeneous population of proteins and other biological materials. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not show significant binding to other proteins present in the sample. Specific binding to an antibody under such conditions can require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to a protein with an amino acid sequence encoded by any of the nucleic acid sequences of the invention can be selected to obtain antibodies specifically immunoreactive with that protein and not with unrelated proteins.

The use of a molecular cloning approach to generate antibodies, particularly monoclonal antibodies, and more particularly single chain monoclonal antibodies, are also provided. The production of single chain antibodies has been described in the art. See, e.g., U.S. Patent No. 5,260,203. For this approach, combinatorial immunoglobulin phagemid libraries are prepared from RNA isolated from the spleen of the immunized animal, and phagemids expressing appropriate antibodies are selected by panning on endothelial tissue. The advantages of this approach over conventional hybridoma techniques are that approximately  $10^4$  times as many antibodies can be produced and screened in a single round, and that new specificities are generated by heavy (H) and light (L) chain combinations in a single chain, which further increases the chance of finding appropriate antibodies. Thus, an antibody of the present invention, or a "derivative" of an antibody of the present invention, pertains to a single polypeptide chain binding molecule which has binding specificity and affinity substantially similar to the binding specificity and affinity of the light and heavy chain aggregate variable region of an antibody described herein.

The term "immunochemical reaction", as used herein, refers to any of a variety of immunoassay formats used to detect antibodies specifically bound to a particular protein, including but not limited to competitive and

non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, *in situ* immunoassays (e.g.,  
5 using colloidal gold, enzyme or radioisotope labels), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. See Harlow & Lane (1988) for a description of immunoassay formats and  
10 conditions.

#### I.E. Protein Binding Assays

The term "binding" refers to an affinity between two molecules, for example, a ligand and a receptor. As used herein, "binding" means a preferential binding of one molecule for another in a mixture of molecules.  
15 The binding of the molecules can be considered specific if the binding affinity is about  $1 \times 10^4 \text{ M}^{-1}$  to about  $1 \times 10^6 \text{ M}^{-1}$  or greater. Binding of two molecules also encompasses a quality or state of mutual action such that an activity of one protein or compound on another protein is inhibitory (in the case of an antagonist) or enhancing (in the case of an agonist). Exemplary  
20 protein binding assays include but are not limited to Fluorescence Correlation Spectroscopy (FCS), Surface-Enhanced Laser Desorption/Ionization time-of-flight mass spectrometry (SELDI-TOF), and Biacore, each described further herein below.

Fluorescence Correlation Spectroscopy (FCS) measures the average  
25 diffusion rate of a fluorescent molecule within a small sample volume (Madge et al. (1972) *Phys Rev Lett* 29:705-708; Maiti et al. (1997) *Proc Natl Acad Sci USA*, 94:11753-11757). The sample size can be as low as  $10^3$  fluorescent molecules and the sample volume as low as the cytoplasm of a single bacterium. The diffusion rate is a function of the mass of the molecule  
30 and decreases as the mass increases. FCS can therefore be applied to protein-ligand interaction analysis by measuring the change in mass and therefore in diffusion rate of a molecule upon binding. In a typical

experiment, the target to be analyzed is expressed as a recombinant protein with a sequence tag, such as a poly-histidine sequence, inserted at the N-terminus or C-terminus. The expression takes place in *E. coli*, yeast or mammalian cells. The protein is purified using chromatographic methods.

5 For example, the poly-histidine tag can be used to bind the expressed protein to a metal chelate column such as  $\text{Ni}^{2+}$  chelated on iminodiacetic acid agarose. The protein is then labeled with a fluorescent tag such as carboxytetramethylrhodamine or BODIPY<sup>TM</sup> (Molecular Probes, Eugene, Oregon). The protein is then exposed in solution to the potential ligand, and  
10 its diffusion rate is determined by FCS using instrumentation available from Carl Zeiss, Inc. (Thornwood, New York). Ligand binding is determined by changes in the diffusion rate of the protein.

Surface-Enhanced Laser Desorption/Ionization (SELDI) was developed by Hutchens & Yip (1993) *Rapid Commun Mass Spectrom* 7:576-  
15 580). When coupled to a time-of-flight mass spectrometer (TOF), SELDI provides a means to rapidly analyze molecules retained on a chip. It can be applied to ligand-protein interaction analysis by covalently binding the target protein on the chip and analyzing by MS the small molecules that bind to this protein (Worrall et al. (1998) *Anal Biochem* 70:750-756). In a typical  
20 experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the SELDI chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via, for example, a  
25 delivery system able to pipet the ligands in a sequential manner (autosampler). The chip is then washed in solutions of increasing stringency, for example a series of washes with buffer solutions containing an increasing ionic strength. After each wash, the bound material is analyzed by submitting the chip to SELDI-TOF. Ligands that specifically  
30 bind the target are identified by the stringency of the wash needed to elute them.



Biacore relies on changes in the refractive index at the surface layer upon binding of a ligand to a protein immobilized on the layer. In this system, a collection of small ligands is injected sequentially in a 2-5 microliter cell, wherein the protein is immobilized within the cell. Binding is  
5 detected by surface plasmon resonance (SPR) by recording laser light refracting from the surface. In general, the refractive index change for a given change of mass concentration at the surface layer is practically the same for all proteins and peptides, allowing a single method to be applicable for any protein (Liedberg et al. (1983) *Sensors Actuators* 4:299-304;  
10 Malmquist (1993) *Nature* 361:186-187). In a typical experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the Biacore chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then  
15 exposed to the potential ligand via the delivery system incorporated in the instruments sold by Biacore (Uppsala, Sweden) to pipet the ligands in a sequential manner (autosampler). The SPR signal on the chip is recorded and changes in the refractive index indicate an interaction between the immobilized target and the ligand. Analysis of the signal kinetics of on rate  
20 and off rate allows the discrimination between non-specific and specific interaction.

#### I.F. Transgenic animals

It is also within the scope of the present invention to prepare a transgenic animal to mutagenize the MS4A locus or to express a transgene  
25 comprising nucleic acid sequences of the present invention. The term "transgenic animal", indicates an animal comprising a germline insertion of a heterologous nucleic acid. Transgenic animals of the present invention are understood to encompass not only the end product of a transformation method, but also transgenic progeny thereof.

30 The term "transgene", as used herein indicates a heterologous nucleic acid molecule that has been transformed into a host cell. For intended use in the creation of a transgenic animal, the transgene includes

genomic sequences of the host organism at a selected locus or site of transgene integration to mediate a homologous recombination event. A transgene further comprises nucleic acid sequences of interest, for example a targeted modification of the gene residing within the locus, a reporter gene,  
5 or a expression cassette, each defined herein above.

Transgene integration can be used to create gene mutations, including “knock-out”, “knock-in”, or a “knock-down” mutations. Representative approaches are disclosed in the Examples presented below. The term “knock-out” refers to a homologous recombination event that  
10 renders a gene inactive. Gene knock-out is generally accomplished by integration of the transgene at a chromosomal loci, thereby interrupting a gene residing at that loci. The term “knock-in” refers to *in vivo* replacement at a targeted locus. Knock-in mutations can modify a gene sequence to create a loss-of-function or gain-of-function mutation. The term “gene  
15 knock-down” refers to a homologous recombination event wherein the transgene partially eliminates gene function. A knock-down animal can be created by transgenic expression of an antisense molecule, wherein a transgene comprising the antisense sequence and a relevant promoter are integrated into the genome at a non-essential loci. Expression of the  
20 antisense or ribozyme molecule disrupts the corresponding gene function, although this disruption is generally incomplete (Luyckx et al. (1999) *Proc Natl Acad Sci U S A* 96(21):12174-12179).

Conditional mutation can be accomplished using transgenic methods in combination with the Cre-recombinase system in mice. Briefly, in one  
25 instance, a transgenic mouse is derived that expresses Cre-recombinase under the direction of an inducible promoter. A second transgenic mouse bears a mutation of a gene of interest as well as a lox-P-flanked endogenous gene sequence. Such transgenic mice are mated, the resulting progeny having both the Cre-recombinase and lox-P-flanked transgenes. Induction  
30 of Cre recombinase catalyzes excision of the lox-P-flanked transgene, thereby excising a portion of the endogenous gene sequence and revealing the mutated sequence. Conditional knockout can be varied according to the

temporal and spatial features of Cre recombinase expression, inherent in the selection of a promoter to drive Cre recombinase. See Postic et al. (1999) *J Biol Chem* 275(1):305-315; and Sauer (1998) *Methods* 14(4):381-392.

Transgenes can also be used for heterologous expression in a host  
5 organism without generating phenotypically apparent mutations. By this method, nucleotide sequences of interest are introduced into the genome at a nonessential loci, whereby insertion alone does not disrupt an essential gene function. Optionally, expression of the transgene can generate a gain-of-function or ectopic function phenotype.

10 Techniques for the preparation of transgenic animals are known in the art. Exemplary techniques are described in U.S. Patent No. 5,489,742 (transgenic rats); U.S. Patent Nos. 4,736,866, 5,550,316, 5,614,396, 5,625,125 and 5,648,061 (transgenic mice); U.S. Patent No. 5,573,933 (transgenic pigs); 5,162,215 (transgenic avian species) and U.S. Patent No.  
15 5,741,957 (transgenic bovine species). Briefly, nucleotide sequences of interest are cloned into a vector, and the construct is transformed into a germ cell. In the germ cell, a chromosomal rearrangement event takes place wherein the nucleic acid sequences of interest are integrated into the genome of the germ cell by homologous recombination. Fertilization and  
20 propagation of the transformed germ cell results in a transgenic animal. Homozygosity of the mutation is accomplished by intercrossing.

#### I.G. Therapeutic Methods

The present invention further provides methods for discovering substances that can be used as pharmaceutical compositions. The term  
25 "pharmaceutical composition" or "drug" as used herein, each refer to any substance having a biological activity. Substances discovered by methods of the present invention include but are not limited to polypeptide, proteins, peptides, chemical compounds, and antibodies.

A composition of the present invention is typically formulated using  
30 acceptable vehicles, adjuvants, and carriers as desired.

Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution, and isotonic sodium chloride solution. In

addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono- or di-glycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectable compositions.

5           Injectable preparations, for example sterile injectable aqueous or oleaginous suspensions, are formulated according to the known art using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation can also be a sterile injectable solution or suspension in a nontoxic diluent or solvent, for example 1,3-butanediol.

10           A vector can be used as a carrier, for example an adenovirus vector, can be used for gene therapy methods. The vector is purified to sufficiently render it essentially free of undesirable contaminants, such as defective interfering adenovirus particles or endotoxins and other pyrogens such that it does not cause any untoward reactions in the individual receiving the vector  
15       construct. A preferred means of purifying the vector involves the use of buoyant density gradients, such as cesium chloride gradient centrifugation.

          A transfected cell can also serve as a carrier. By way of example, a liver cell can be removed from an organism, transfected with a nucleic acid sequence of the present invention using methods set forth above and then  
20       the transfected cell returned to the organism (e.g. injected intra-vascularly).

          Monoclonal antibodies or polypeptides of the invention can be administered parenterally by injection or by gradual infusion over time. Although the tissue to be treated can typically be accessed in the body by systemic administration and therefore most often treated by intravenous  
25       administration of therapeutic compositions, other tissues and delivery means are provided where there is a likelihood that the tissue targeted contains the target molecule and are known to those of skill in the art.

          Representative antibodies for use in the present invention are intact immunoglobulin molecules, substantially intact immunoglobulin molecules,  
30       single chain immunoglobulins or antibodies, those portions of an immunoglobulin molecule that contain the paratope, including antibody

fragments. It is within the scope of the present invention that a monovalent modulator can optionally be used.

Methods of preparing "humanized" antibodies are generally well known in the art, and can readily be applied to the antibodies of the present invention. Humanized monoclonal antibodies offer particular advantages over monoclonal antibodies derived from other mammals, particularly insofar as they can be used therapeutically in humans. Specifically, humanized antibodies are not cleared from the circulation as rapidly as "foreign" antigens, and do not activate the immune system in the same manner as foreign antigens and foreign antibodies.

With respect to the therapeutic methods of the present invention, a preferred subject is a vertebrate subject. A preferred vertebrate is warm-blooded; a preferred warm-blooded vertebrate is a mammal. A preferred mammal is a mouse or, most preferably, a human. As used herein and in the claims, the term "patient" includes both human and animal patients. Thus, veterinary therapeutic uses are provided in accordance with the present invention.

Also provided is the treatment of mammals such as humans, as well as those mammals of importance due to being endangered, such as Siberian tigers; of economical importance, such as animals raised on farms for consumption by humans; and/or animals of social importance to humans, such as animals kept as pets or in zoos. Examples of such animals include but are not limited to: carnivores such as cats and dogs; swine, including pigs, hogs, and wild boars; ruminants and/or ungulates such as cattle, oxen, sheep, giraffes, deer, goats, bison, and camels; and horses. Also provided is the treatment of birds, including the treatment of those kinds of birds that are endangered and/or kept in zoos, as well as fowl, and more particularly domesticated fowl, *i.e.*, poultry, such as turkeys, chickens, ducks, geese, guinea fowl, and the like, as they are also of economical importance to humans. Thus, provided is the treatment of livestock, including, but not limited to, domesticated swine, ruminants, ungulates, horses, poultry, and the like.



As used herein, the term “experimental subject” refers to any subject or sample in which the desired measurement is unknown. The term “control subject” refers to any subject or sample in which a desired measure is unknown.

5           As used herein, an “effective” dose refers to a dose(s) administered to an individual patient sufficient to cause a change in MS4A activity. One of ordinary skill in the art can tailor the dosages to an individual patient, taking into account the particular formulation and method of administration to be used with the composition as well as patient height, weight, severity of  
10 symptoms, and stage of the biological condition to be treated. Such adjustments or variations, as well as evaluation of when and how to make such adjustments or variations, are well known to those of ordinary skill in the art of medicine.

A therapeutically effective amount can comprise a range of amounts.  
15 One skilled in the art can readily assess the potency and efficacy of a MS4A modulator of this invention and adjust the therapeutic regimen accordingly. A modulator of MS4A biological activity can be evaluated by a variety of means including the use of a responsive reporter gene, interaction of MS4A polypeptides with a monoclonal antibody, analysis of cell subpopulations,  
20 and measurement of  $[Ca^{2+}]_i$  levels, each technique described herein.

Additional formulation and dose techniques have been described in the art, see for example, those described in U.S. Patent Nos. 5,326,902 and 5,234,933, and International Publication No. WO 93/25521.

For the purposes described above, the identified substances can  
25 normally be administered systemically, parenterally, or orally. The term “parenteral” as used herein includes intravenous, intra-muscular, intra-arterial injection, or infusion techniques. Other compositions for administration include liquids for external use, and endermic liniments (ointment, etc.), suppositories, and pessaries which comprise one or more of  
30 the active substance(s) and can be prepared by known methods.

## II. CD20 Gene Family Members

### II.A. Identification of CD20 Gene Family Members

The present invention provides MS4A nucleic acid and polypeptide sequences. Preferably, a MS4A gene comprises the sequence set forth as  
5 any one of the odd-numbered SEQ ID NOs:1-37, a nucleic acid molecule that is substantially similar to any one of the odd-numbered SEQ ID NOs:1-37, or a nucleic acid molecule comprising a 20 base pair nucleotide sequence that is identical to a contiguous 20 base pair sequence of any one of the odd-numbered SEQ ID NOs:1-37.

10 To identify new CD20 gene family members, the human and mouse CD20 amino acid sequences (Tedder et al., 1988a; Tedder et al., 1988b) were used to search the translated GenBank databases, including expressed sequence tags, using the BLAST program (Altschul et al., 1997). Among 337 homologous sequences identified, at least 17 novel genes  
15 expressed by mouse, human, and pig had predicted amino acid sequences homologous to CD20. Complete coding regions were predicted using overlapping nucleotide sequences obtained from sequenced ESTs and cDNAs that corresponded to unique, near full-length transcripts in humans and mice (Figure 1). All nucleotide sequences were verified by sequencing  
20 multiple near full-length cDNAs isolated by applicants and 40 cDNAs obtained from the ATCC (American Tissue Culture Collection, Bethesda, Maryland, USA). In addition, a pig cDNA and its human counterpart homologous to CD20 were identified as GenBank submissions AJ236932.1 and AK000224, respectively. In total, unique cDNA clones were identified  
25 that encode at least 16 distinct full-length CD20-like proteins.

Complete cDNA sequences encoding the human and mouse MS4A family members (*MS4A1*, *-A2*, *-A3*, *-A4A*, *-A5*, *-A6A*, *-A7*, *-A8B* and *-A12*) were also used to search the GenBank human genomic database (htgs;  
<http://www.ncbi.nlm.nih.gov/blast/>) using the BLAST program (Altschul et al.,  
30 1997), as further described in Example 2. Two-hundred-twenty different contigs or distinct genomic DNA sequences were identified in the database of unfinished human genomic sequences that were either identical or similar

to MS4A family members. These sequences were predominantly derived from sixteen partially sequenced bacterial artificial chromosomes (BACs) that spanned 400-500 kb of human chromosome 11q12 (Table 1). Based on known cDNA sequences of MS4A family members, we were able to order  
5 and arrange these genomic sequences into overlapping continuous DNA segments. Since many of the contigs identified were overlapping, it was thereby possible to assemble long DNA sequences that encoded entire MS4A genes or portions of MS4A genes. Gaps between exon encoding DNA sequences were filled in many cases by additional sequence homology  
10 searches using DNA sequences found at the ends of gaps. When sequence differences were observed between different overlapping DNA fragments, consensus sequences were used or PCR primers were generated, that portion of genomic DNA was then amplified and sequenced to resolve ambiguous sequences.

15 BLAST analysis of the htgs phase 1 or phase 2 human genomic DNA sequences encoding MS4A cDNAs and the assembled and annotated human genomic sequence thereof, as disclosed herein, revealed the presence of each known human MS4A family member. In addition, three putative genes encoding unique MS4A family members were identified that  
20 localized to the q12-13.1 region of human chromosome 11. Complete coding regions were predicted using overlapping nucleotide sequences obtained from sequenced ESTs and cDNAs and by comparison of gene structure, described further herein below (Figure 2).

By identifying sequences that correlated with different MS4A genes in  
25 each BAC (Table 1), and by the assembly of minimal genomic DNA lengths that could encode each *MS4A* gene (Figure 2), we used the overlapping BACs to identify the order of the MS4A genes on chromosome 11q12 (Figure 6). This analysis also allowed us to determine the direction of gene transcription for most MS4A genes. Furthermore, the MS4A cDNA  
30 sequences, disclosed herein, were used to assemble genomic clones set forth as SEQ ID NOs:73-81. In some cases, multiple MS4A genes could be aligned within a continuous genomic sequence. For example, the genomic

sequence set forth as SEQ ID NO:77 comprises both the *MS4A4E* and *MS4A6A* genes. Similarly, the genomic region set forth as SEQ ID NO:79 comprises three *MS4A* genes: *MS4A7*, *MS4A5*, and *MS4A12*.

5       The *MS4A4E* gene encodes 660 bp of translated sequence (Figure 3), contained within at least seven exons (Figure 2). Exons were identified based on their sequence similarities with *MS4A4A* sequences and the identification of canonical splice-donor and -acceptor sites (Aebi & Weissmann, 1987). The *MS4A4E* gene sequence was at least 23,379 base pairs in length, if counted from the putative translation initiation ATG site until  
10       the TGA translation termination stop site (Figure 2). An exon encoding the putative 5' untranslated region of *MS4A4E*, was highly homologous with the corresponding sequence in *MS4A4A* cDNAs (disclosed herein). This sequence homology extended for >7 kbp upstream from this putative exon and also included upstream repetitive Alu elements. Representative  
15       upstream homologous sequences are shown in Figure 3. Similar sequence homologies were identified in the 3' untranslated regions of *MS4A4E* and *MS4A4A*, which extended beyond the poly-A attachment signal sequences (Figure 3). Based on the sequence similarities in translated and untranslated exons, it appears that the *MS4A4E* and *MS4A4A* genes  
20       resulted from a recent gene duplication event.

      The *MS4A6E* gene encodes 441 bp of translated sequence (Figure 4), contained within at least four exons (Figure 2). Exons were identified based on their sequence similarities with *MS4A6A* cDNA sequences and the identification of canonical splice-donor and -acceptor sites (Aebi &  
25       Weissmann, 1987). In addition, the predicted gene sequences matched those found in three cDNA clones that were sequenced (ATCC Nos. 3704466, 1852248 and 3557769). The *MS4A6E* gene was at least 5,060 bp in length, if counted from the putative translation initiation ATG site until the TGA translation termination codon (Figure 2). The *MS4A6E* gene lacks  
30       exons that encode the first two membrane spanning domains present in most *MS4A* family proteins (Figures 2 and 7). An exon homologous with the 5' untranslated region of *MS4A6A* cDNAs was not identified within 7,629 bp

of sequence upstream of the exon encoding the translation initiation site of *MS4A6E*. However, there was a canonical 3' splice region upstream of the ATG initiation codon located at identical positions in the *MS4A6E* and *MS4A6A* genes. Similar sequence homologies were identified in the 3' untranslated regions of *MS4A6E* and *MS4A6A* that extend beyond the sequence shown in Figure 4. Based on the sequence similarities in translated and untranslated exons, it appears that the *MS4A6E* and *MS4A6A* genes represent a recent gene duplication event, although several exons encoding translated sequence were lost in the *MS4A6E* gene (Figure 2).

The *MS4A10* gene encodes 726 bp of translated sequence (Figure 5), contained within at least six exons (Figure 2). Exons were identified based on their sequence similarities with mouse *MS4a10* cDNA sequences and the identification of canonical splice-donor and -acceptor sites (Aebi & Weissmann, 1987). The *MS4A10* gene was at least 8,183 bp in length if counted from the putative translation initiation ATG site until the TGA translation termination stop site (Figure 2). An exon homologous with the 5' untranslated region of mouse *MS4a10* cDNAs was not identified within 8,829 bp of sequence upstream of the exon encoding the translation initiation site of *MS4A10*. However, there was a canonical 3' splice region upstream of the ATG initiation codon located at identical positions in the *MS4A10* and *MS4a10* genes. Modest sequence homologies were identified in the 3' untranslated regions of *MS4A10* and *MS4a10* (Figure 5).



Table 1  
Human BACs Containing MS4A Genes

BAC	Accession No. <sup>a</sup>	Chromosome	MS4A gene <sup>b</sup>
RP11-206B10	AC009703	15	A4A, A4E, A6A
RP11-21B14	AC013807	unknown	A6A, A2, A3
RP11-24D1	AC015840	unknown	A4A, A5, A6E, A7
RP11-652L5	AC018966	11	A4A, A4E, A6A
RP11-448N3	AC024066	11	A8B
RP11-312N17	AC027599	11	A8B, A10
RP11-196E16	AC027787	15	A5, A1
CMB9-79B2	AP000748	11q23	A10
RP11-804A23	AP000777	11	A10
RP11-736I10	AP000790	11q12	A3
RP11-804B24	AP000934	11	A10
RP11-729B4	AP001034	11q12	A5, A12, A1
CMB9-2M23	AP001181	11q12	A2, A3
CMB9-100I1	AP001257	11q12	A6A, A4E
CMB9-49F18	AP001259	11	A8B
RP11-68H20	AP001986	11q	A10

<sup>a</sup>GenBank Accession number for the indicated BAC.

5 <sup>b</sup>indicates the MS4A gene sequences that mapped to each BAC.

## II.B. MS4A Nomenclature

In collaboration with the Human Gene Nomenclature Committee ([www.gene.ucl.ac.uk/nomenclature/](http://www.gene.ucl.ac.uk/nomenclature/)), this gene family was designated as the MS4A family (Membrane Spanning 4-domain family, subfamily A). The MS4 designation is to accommodate the future identification of genes encoding proteins with a similar structure, yet with unresolved functions. Subfamily A will designate the CD20 family. Using this nomenclature, the CD20 gene was designated as *MS4A1*, *FcεRIβ* as *MS4A2*, and HTm4 as *MS4A3*. Among the 16 novel genes identified, 8 human genes were named *MS4A4A*, *MS4A4E*, *MS4A5*, *MS4A6A*, *MS4A6E*, *MS4A7*, *MS4A8B*, and *MS4A12*. A ninth gene encoded a protein homologous with the single member of the mouse MS4a10 subfamily. This gene was tentatively designated as *MS4A10*. The remaining genes were of mouse or pig origin and were therefore labeled as *MS4a3-MS4a12* based on the nomenclature of homologous genes corresponding to human counterparts. Distinct mouse genes that encoded proteins with highly homologous sequences were designated as *MS4a4B*, *MS4a4C*, *MS4a4D*, and as *MS4a6B*, *MS4a6C*, and *MS4a6D* to signify close homology.

## II.C. MS4A Gene Chromosome Locations

Chromosome locations for the human *MS4A4A*, *MS4A6A*, *MS4A7*, and *MS4A8B* genes were identified in two distinct homology searches. Regions of human *MS4A4A* (bp 1286-1588), *MS4A6A* (bp 682-1106), *MS4A7* (bp 502-941), *MS4A7* (bp 1015-1177), and *MS4A8B* (bp 1007-1350), were 98%, 98%, 97%, 99% and 97% identical with human STS genomic sequence tag sites, WI-11578, SHGC-36634, WI-12101, WIAF-3856, and WI-14145, respectively (<http://www.ncbi.nlm.nih.gov/blast>). These genomic sequence tag sites are located on human chromosome 11 at Genomic Database locus D11S1357-D11S913, which maps to 11q12-13 (<http://www.ncbi.nlm.nih.gov/genemap>). These mapping results were confirmed using the UniGene collection at the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/Genemap98/>) for expressed sequence tags identical to human *MS4A4A*, *MS4A6A*, *MS4A7*,

*MS4A8B* sequences. By this analysis, at least 7 of the 9 currently identified human *MS4A* genes are clustered.

The organization of the 12 *MS4A* genes on human chromosome 11 was determined by identifying sequenced human genomic DNA fragments (contigs of different lengths) from 15 BAC clones (Table 1). Contiguous DNA segments for each BAC were constructed based on human *MS4A* exon and cDNA sequences, and overlapping contigs. Although some gaps were present in *MS4A* gene introns (Figure 2) or between *MS4A* genes, the relative position of each gene on chromosome 11q12-13.1 was determined (Figure 6). *MS4A1* was located in a telemetric region of 11q12-13.1 compared with *MS4A2* and *MS4A3*. Seven *MS4A* genes were located in between *MS4A1* and *MS4A2*. Two other *MS4A* genes, *MS4A8B* and *MS4A10* were centromeric to *MS4A2* and *MS4A3*, although the distance between these genes was not determined. Interestingly, *MS4A6A*, *MS4A4E*, *MS4A4A* and *MS4A6E* were arranged linearly suggesting that these genes might have arisen through the duplication of a single genomic element. It is envisioned that this genetic locus extends further and contains additional *MS4A* genes.

#### II.A. *MS4A* Gene Structure

Complete coding region sequences were verified for each deduced protein, except for the *MS4a3* cDNA that was not full-length (Figure 1). Proposed ATG translation initiation codons were based on the translation initiation consensus sequence, ANNATG (Kozak (1986) *Cell* 44:283-292), and the existence of in-frame upstream translation stop codons in most cases. Whether the first or second ATG codon in mouse *MS4a8B* was used for translation initiation was unknown although the second ATG was identical with the start codon of human *MS4A8B* (Figure 7).

Poly(A) attachment signal sequences were identified in the proximal 3' untranslated regions of each gene product except *MS4A6A*, *MS4A6E*, *MS4A10*, and *MS4a6C*. Two poly(A) signal sequences were found in *MS4a4D*, *MS4A5*, and *MS4a10* transcripts, while four were observed in *MS4A4A* transcripts.

The disclosed MS4A cDNAs were further used to annotate the genomic sequence derived from BAC clones. Annotated features include definition of coding regions, intron|exon junctions, sequences upstream of the initial coding region of each gene that comprise the promoter region, and  
5 other adjacent sequences that could also comprise gene regulatory elements. Representative methods for further characterizing a MS4A promoter region are disclosed in Example 9.

Annotation of human MS4A genomic regions (SEQ ID NOs:73-81), as disclosed herein, enabled a comparison of gene structure among MS4A  
10 genes. The overall domain organization of each MS4A gene was similar (Figures 2 and 7). All exon|intron|exon boundaries were consistent with consensus splice-donor and -acceptor sequences unless otherwise indicated, with exon|GTGAGT-intron-CAG|exon sequences in most cases (Aebi & Weissmann, 1987). In addition, the splice junctions for all translated  
15 exons were located after the third nucleotide in each codon. Most MS4A proteins were encoded by 6 exons except MS4A2, MS4A5, and MS4A6E (Figure 2 and 7). In these exceptions: the N-terminal cytoplasmic domain of MS4A2 was encoded by two exons (Küster et al., 1992); the *MS4A5* and *MS4A6E* genes did not encode C-terminal cytoplasmic domains; and the  
20 *MS4A6E* gene had only two membrane spanning domains. Intron lengths demonstrated wide variation from 181 bp in *MS4A12* to 13,731 bp in *MS4A5*. In some cases however, exact intron lengths were not determined; *MS4A3*, *MS4A4*, and *MS4A12* (Figure 2). Distances between translation initiation and termination codons were determined for most MS4A genes;  
25 with *MS4A6E* being the smallest (5,060 bp) and *MS4A4E* being the longest (23,379 bp) genes (Figure 6). Thus, the intron|exon organization of all MS4A family members is consistent with the high degree of conservation within this gene family.

There were no amino-terminal signal sequences, although all MS4A  
30 proteins contained hydrophobic regions of sufficient length to pass through the membrane at least four times. Notable was a marked clustering of charged residues at both ends of the putative transmembrane domains,

some of which were highly conserved. In some cases, the first and second putative transmembrane domains of MS4A proteins were a continuous stretch of hydrophobic amino acids without an obvious inter-transmembrane hydrophilic bridge. By contrast, MS4A4A and MS4A7 had 6 to 7 hydrophilic amino acids inserted between the first and second hydrophobic domains. In human MS4A4A and mouse MS4a4B, MS4a4C, and MS4a4D, an extensive hydrophobic region followed the fourth putative membrane-spanning domain. Thus, the overall structure of MS4A family members was well conserved.

#### 10        II.E.    MS4A Gene Splice Variants

Among the MS4A cDNAs sequenced and EST sequences analyzed, multiple splice variants were identified that encoded variant MS4A proteins. In most cases, exons were spliced out, which generated truncated protein products. Potential splice variants of the *MS4A4A*, *MS4A5*, *MS4A6A*, and *MS4A7* genes were identified. Whether these alternatively spliced variants produce functional proteins has yet to be determined.

Two splice variations of the *MS4A4A* gene were identified during an analysis of *MS4A4A* mRNA expression by lymphoblastoid cell lines. Most of the hematopoietic cell lines examined expressed transcripts encoding a full-length MS4A4A protein as shown in Figure 7. However, a second smaller transcript was also expressed in most cases that contained a potential exon deletion of 158 nucleotides. This was a frequent event since 40% of *MS4A4A* cDNAs generated from the BJAB B cell line encoded the truncated protein. In addition, the same splicing event was observed in two of five EST sequences that covered this region of the MS4A4A protein. Splicing-out this potential exon deleted the third membrane-spanning domain and the second extracellular loop from the full-length protein (positions 110-163, Figure 3). Of interest, this splicing event fused the first/second membrane spanning domains with the fourth membrane spanning domain. However, the fourth transmembrane spanning domain in MS4A4A is followed by another hydrophobic region of sufficient length to traverse the membrane (disclosed herein). This suggests that differential splicing can generate an



alternative MS4A4A protein with four membrane spanning domains lacking a significant extracellular domain.

In the case of the *MS4A5* gene, two of nine *MS4A5* EST sequences analyzed (GenBank Accession Nos. AA411806 and AA781801) encoded a  
5 splice variant that preserved the reading frame of the transcript. In both sequences, the exon encoding the third membrane-spanning domain and the second extracellular loop from the full-length protein (TM3, Figure 1) was spliced out using normal splice-donor and -acceptor sequences, which deleted 51 amino acids (114-164) from the full length protein (Figure 7).  
10 This deletion resulted in a protein with the first/second membrane spanning domains fused with the fourth predicted membrane-spanning domain. Thus, the truncated MS4A5 protein would possess three membrane-spanning domains with an extracellular carboxyl-terminal domain.

A novel splicing event was observed in the *MS4A6A* gene which  
15 resulted in a truncated protein. A novel splice donor site (CAG T<sup>683</sup>|GT GAG T) is located within the exon encoding the TM3/extracellular loop domains (Figure 4). This cryptic splice donor site was spliced with the normal 3' splice acceptor site of the exon encoding the TM4 domain, which thereby deletes nucleotides 684-787 from *MS4A6A* transcripts (Figure 4). Since  
20 there was an extra T introduced into the codon sequence due to this alternative splicing event, there was a frameshift in the coding sequence. This potentially results in the attachment of a novel 30 amino acid sequence (-WNSLSDADLHSAGILPSCAHCCAAVETGLL) that is not predicted to be hydrophobic. Thus, the variant MS4A protein would be 70 amino acids  
25 shorter and would lack the fourth membrane-spanning and cytoplasmic domains. This alternative splicing event was found in 3 of 29 EST sequences that encoded this region (GenBank Accession Nos. AI278475, AA461046, and AA448335) and in one cDNA clone (GenBank Accession No. AB013104).

30 Splice variation in *MS4A7A* transcripts produces two distinct protein products in addition to the presumably normal protein. In one case, a splice variation in *MS4A7A* transcripts produces a protein product similar in

structure to the MS4A6E protein. The exon encoding the first/second membrane spanning domains (amino acids 50-94, Figure 7) was deleted in 2 of 4 MS4A7 EST sequences analyzed (GenBank Accession Nos. N42191 and R11179) that cover this region. Thus, the protein product would have a longer N-terminal cytoplasmic domain and only two membrane spanning domains. In the second case, the exon encoding the fourth membrane-spanning domain (amino acids 183-216) was deleted in 2 EST sequences (GenBank Accession Nos. R11180 and AI188478) out of 18 sequences analyzed (Figure 7).

#### 10        II.F. MS4A Gene Polymorphisms

Putative polymorphisms were identified in the MS4A6A gene. Two nucleotide substitutions were found in cDNA clone ATCC No. 499181 and in 13 of 38 EST sequences analyzed (Figure 1). The first substitution was at nucleotide 373 that exchanged a C for a T, which did not alter the amino acid sequence. The second substitution resulted in a Ser in place of Thr at amino acid 185. In addition, a third substitution was found in 4 of the 38 EST sequences analyzed where a Ser was substituted in place of an Ala at amino acid position 183. This substitution was paired with a Ser to Thr substitution at amino acid position 185 in half of the clones analyzed. These differences most likely represent common sequence polymorphisms since they were observed in multiple independent cDNA clones. Based on our genetic DNA analysis, it is unlikely that these differences could represent transcripts from distinct genes that are almost identical in coding sequence.

As with the MS4A6A gene (disclosed herein), potential gene polymorphisms were observed in MS4A6E. Three cDNA clones representing partial transcripts were sequenced completely on both strands. The predicted MS4A6E gene product and one cDNA clone (ATCC No. 3704466) had identical sequences. However, the ATCC No. 3557769 cDNA had a nucleotide substitution at position 314 (Figure 4) that exchanged a T for a C, which did not alter the predicted amino acid sequence. The ATCC No.1852248 cDNA clone had the longest insert that starts at nucleotide position 60 and ended at position 661 as shown in Figure 4. This cDNA had

a substitution at nucleotide 153 that exchanged a G for a T, which resulted in a Phe in place of Val at amino acid 47 (Figure 4). Therefore, sequence polymorphisms can exist within the *MS4A6E* gene.

Other potential polymorphisms were observed in other MS4A family members based on consistent nucleotide variations found in *MS4A4E* sequences.

The assembly and annotation of genomic sequences comprising MS4A genes in the region of human chromosome 11q12-13.1, disclosed herein for the first time, provide source material for identification of polymorphisms that are linked to MS4A genes. Such polymorphisms can include single nucleotide polymorphisms as disclosed within the *MS4A6A* and *MS4A6E* coding region sequences. In addition, polymorphisms within or genetically linked to MS4A genes can also comprise restriction length polymorphisms (RFLPs) (Lander & Botstein (1989) *Genetics* 121:185-199), short tandem repeat polymorphisms (STRPs), short sequence length polymorphisms (SSLPs) (Dietrich et al. (1996) *Nature* 380:149-152), amplified fragment length polymorphisms (AFLPs) (Latorra et al. (1994) *PCR Methods Appl* 3(6):351-358), and microsatellite markers (Schalkwyk et al. (1999) *Genome Res* 9:878-887). Identification of polymorphisms within an isolated DNA molecule are known to one of skill in the art.

#### II.G. MS4A Proteins

The MS4A genes encoded proteins of 16-29 kDa (Table 2).

Table 2  
MS4A Family Members

Human		Mouse		Human/Mouse
Name	kDa	Name	kDa	Homology
		MS4a3		63% (partial)
MS4A4A	23			
		Ms4a4B	24	41%
		Ms4a4C	24	44%
		Ms4a4D	24	40%
MS4A4E	24			
MS4A5	22			
MS4A6A	27			
		Ms4a6B	27	52%
		Ms4a6C	24	51%
		Ms4a6D	26	53%
MS4A6E	16			
MS4A7	26	MS4a7	26	53%
MS4A8B	26	MS4a8B	29	63%
MS4A10	27	MS4a10	29	52%
MS4A12	26	MS4a12(pig)	26	60%

<sup>a</sup>Predicted molecular weights for the new MS4A family members and the  
5 percentage amino acid sequence identity between deduced MS4A and  
MS4a proteins.

Comparisons between CD20 and the predicted amino acid sequences for human MS4A4A, MS4A5, MS4A6A, MS4A7, MS4A8B, and MS4A12 revealed 23-29% amino acid sequence identity (Figure 7). The highest degree of identity was found in the first three transmembrane domains with multiple regions of conserved amino acids. In particular, the amino acid sequences LGAXQI (SEQ ID NO:57) and LSLG (SEQ ID NO:58) were common within the first transmembrane domain, GYPFWG (SEQ ID NO:60) and FIISGSLS (SEQ ID NO:61) were common in the second domain, and SLX<sub>2</sub>NX<sub>2</sub>SX<sub>3</sub>AX<sub>2</sub>G (SEQ ID NO:62) was found in the third transmembrane domain. The first and second transmembrane domains of MS4A8B were 46% identical in amino acid sequence with human CD20, 41% identical with FcεRIβ, and 39% identical with HTm4. The MS4A4A, MS4A5, MS4A6A, and MS4A7 proteins were most homologous in their first and second transmembrane domains with the human FcεRIβ chain, with 37-46% amino acid sequence identity. There was large variation between MS4A proteins in the N- and C-terminal cytoplasmic domains. However, Pro residues were significantly over-represented within the N- and C-terminal cytoplasmic domains of most MS4A family members. There was some sequence identity in the first potential extracellular loop that was ~13 amino acids in length for each protein. By contrast, the second predicted extracellular loop ranged from 10-46 amino acids in length with diverse sequences.

The putative *MS4A4E* gene encodes a 220 amino acid protein of 23.8 kDa with a predicted amino acid sequence that is 76% identical with the MS4A4A protein (Figure 3). Consistent with other MS4A proteins, the most significant homologies between MS4A4E and other MS4A family members were found in the membrane spanning domains (Figure 7). Common amino acid motifs were readily visualized such as KXLGAIQI (SEQ ID NO:57), GYPXWG (SEQ ID NO:60), and SGXLSI (SEQ ID NO:59) in the first and second hydrophobic regions that represent potential transmembrane regions. The intracellular N- and C-terminal domains were highly conserved



between MS4A4E and MS4A4A, but were divergent from other family members.

The putative *MS4A6E* gene encodes a 147 amino acid protein of 15.9 kDa with a predicted amino acid sequence that is 78% identical with the MS4A6A protein (Figure 4). The most significant homologies between MS4A6E and other MS4A family members were found in the membrane spanning domains, although MS4A6E only had two (TM3 and TM4) membrane-spanning domains (Figures 4 and 7). The putative second extracellular loops of MS4A6E and MS4A6A were of identical length (Figure 4). Common amino acid motifs were readily visualized in the hydrophobic regions that represent potential transmembrane regions. The intracellular N-terminal domain was highly conserved between MS4A6E and MS4A6A, but were divergent from other family members. MS4A6E protein also lacks a C-terminal cytoplasmic domain (Figure 4).

The putative *MS4A10* gene encodes a translated 241 amino acid protein of 26.9 kDa with a predicted amino acid sequence that is 52% identical with the mouse MS4a10 protein (Figure 5). The most significant homologies between MS4A10 and MS4a10 were found in the membrane spanning domains and the putative second extracellular loop (Figure 5). Although the N-terminal cytoplasmic domains of MS4A10 and MS4a10 were of similar length, the intracellular N- and C-terminal domains had the lowest sequence homologies among domains. The cytoplasmic C-terminal domain was 28 amino acids shorter in MS4A10 than MS4a10. Nonetheless, based on the sequence similarities of translated regions, it appears that MS4A10 and MS4a10 represent homologous genes that are more similar to one another than other MS4A family members.

Ten novel mouse MS4A proteins were identified that shared 40-63% amino acid sequence identity with their potential human counterparts (Figure 7, Table 2). For comparison, the mouse and human CD20 proteins are 74% identical in amino acid sequence (Tedder et al., 1988a). A single partial cDNA was identified that encoded the mouse homologue for HTm4 (*MS4a3*, Figure 7). The predicted amino terminus of the proposed MS4a3 protein

was 23 amino acids shorter than in the human protein, although their overlapping regions were 63% identical in amino acid sequence. In all cases, the transmembrane domains of the human and mouse MS4A proteins were the most well conserved regions. For example, the human  
5 MS4A8B protein was 78% identical in sequence to MS4a8B in the first 3 transmembrane domains and 68% identical in domain 4. Additional MS4A genes are likely to be identified in humans and mice, including the mouse *MS4A5* homologue.

A UPGMA (unweighted pair group method using arithmetic averages)  
10 tree showing relatedness of deduced MS4A and MS4a protein sequences is depicted in Figure 8.

### III. Methods for Detecting a MS4A Nucleic Acid Molecule

In another aspect of the invention, a method is provided for detecting  
15 a nucleic acid molecule that encodes a MS4A polypeptide. According to the method, a biological sample having nucleic acid material is procured and hybridized under stringent hybridization conditions to a MS4A nucleic acid molecule of the present invention. Such hybridization enables a nucleic acid molecule of the biological sample and the MS4A nucleic acid molecule to  
20 form a detectable duplex structure. Preferably, the MS4A nucleic acid molecule includes some or all nucleotides of any one of the odd-numbered SEQ ID NOs:1-37. Also preferably, the biological sample comprises human nucleic acid material.

#### III.A. Expression of MS4A Family Members in Hematopoietic Cells

25 Since CD20, Fc $\epsilon$ RI $\beta$ , and HTm4 expression are restricted to hematopoietic tissues, MS4A gene transcription was assessed by PCR amplification of cDNA from eleven human hematopoietic cell lines. Like CD20, *MS4A8B* was only expressed by B cell lines (Table 3). *MS4A5* was only expressed by a promonocytic cell line. *MS4A6A* transcripts were  
30 expressed by B cell, myelomonocytic, and erythroleukemia cell lines. *MS4A4A* mRNA was expressed by all cell lines examined, although the relative mRNA levels varied significantly. *MS4A7* was expressed in most,

but not all of the cell lines tested. *MS4A12* transcripts were not detected in these cell lines. Thus, most *MS4A* family members are likely to be expressed in hematopoietic tissues.

ESTs encoding *MS4A* transcripts were isolated from a variety of  
5 different cDNA libraries. *MS4A4A* ESTs were from aorta, brain, breast, heart, kidney, lung, ovary, pancreas, placenta, prostate, stomach, testis, and uterine tissues. *MS4A5* ESTs were only isolated from testis. *MS4A6A* ESTs were from aorta, brain, the central nervous system, colon, gall bladder, heart, kidney, lung, muscle, ovary, pancreas, placenta, prostate, skin,  
10 stomach, tonsil, uterus and embryonic tissues. *MS4A7* ESTs were from lung, kidney, lymphocytes, mammary gland, placenta, spleen, testis, thymus, and uterine tissues. *MS4A8B* ESTs were from brain, lung, uterus and embryonic tissues. A single *MS4A12* EST was isolated from colon. This demonstrates differential *MS4A* gene transcription among lymphoid and  
15 non-lymphoid tissues.

Table 3  
MS4A mRNA Expression by Human Lymphoblastoid Cell Lines

MS4A family member <sup>a</sup>											
Cell lines:	1	2	3	4A	5	6A	7	8B	12	G3PDH	
Pre-B:											
NALM-6	-	-	-	+++	-	-	-	-	-	+++	
B cell:											
BJAB	+++	-	-	+++	-	-	+++	+	-	+++	
DAUDI	+++	-	-	+	-	-	+++	+	-	+++	
SB	+++	-	-	++	-	+++	+++	+	-	+++	
T cell:											
HSB-2	-	-	-	+	-	-	-	-	-	+++	

HUT-78	-	-	-	+	-	-	+	-	-	+++
JURKAT	-	-	-	+	-	-	-	-	-	+++
MOLT15	-	-	-	+	-	-	-	++	-	+++
Myelomonocyte:										
HL60	-	-	+++	++	-	+++	+++	-	-	+++
U937	-	-	+++	+++	+	+	+++	-	-	+++
Erythroleukemia:										
K562	-	+	+++	+++	-	+	-	-	-	+++

<sup>a</sup>Gene transcription was assessed by PCR amplification of cDNA generated from mRNA isolated from each cell type. Values represent the level of PCR product generated relative to the glyceraldehyde-3-phosphate dehydrogenase (G3PDH) control in the separate PCR reactions: -, no specific PCR product detected; +, low levels of the appropriate band were detectable; ++ to +++ appropriate bands of increasing intensity were readily visualized in all samples examined. Identical results were obtained using the different primer pairs for cDNA amplification.



Since most of the MS4A genes are expressed by hematopoietic cells, *MS4A4E*, *MS4A6E* and *MS4A10* transcription were assessed by RT-PCR amplification of cDNA from human hematopoietic cell lines and human tissues. Transcripts from eleven human hematopoietic cell lines were  
5 evaluated; one pre-B cell line (NALM-6), three B cell lines (BJAB, DAUDI, and SB), four T cell lines (HSB-2, HUT-78, JURKAT, and MOLT15), two myelomonocytic lines (HL60 and U937), and one erythroleukemia cell line (K562). In addition, transcripts from eight human tissues were evaluated; colon, ovary, peripheral blood leukocytes, prostate, small intestine, spleen,  
10 testes and thymus. However, *MS4A4E*, *MS4A6E* and *MS4A10* transcripts were not detected in any of these cell lines or tissues.

*MS4A4E*, *MS4A6E*, and *MS4A10* sequences were also used to search the translated GenBank databases using the BLAST program (Altschul et al., 1997). Eleven EST sequences representing *MS4A6E*  
15 transcripts were found that represented nine cDNAs isolated from pooled fetal organ libraries (GenBank Accession Nos. AA382998, AA909515, AA917066, AI222355, AI279944, AI684553, AI699419, AI743473, AI806247), one cDNA from a pooled germ cell tumor library (GenBank Accession No. AI968835), and one cDNA from a colon tumor (GenBank  
20 Accession No. AW951636). EST cDNAs encoding *MS4A4E* or *MS4A10* sequences were not identified. This suggests that *MS4A4E*, *MS4A6E*, and *MS4A10* transcripts are rare among normal tissues or they are primarily expressed during oncogenesis or embryogenesis.

MS4a gene expression by mouse tissues was assessed by Northern  
25 analysis and PCR amplification of cDNAs (Table 4). In most cases assessed, Northern analysis failed to detect specific MS4a transcripts in tissues that revealed transcript production by PCR amplification. These results suggest that MS4a transcripts are only produced by subpopulations of cells within each tissue such that transcript levels were often below the  
30 level of detection by Northern analysis. Nonetheless, *MS4a4B*, *MS4a4C*, and *MS4a6B* transcripts were found at high levels in thymus, spleen and peripheral lymph nodes, with less abundant levels in non-lymphoid tissues.

*MS4a6C* was only expressed by thymus, spleen, PLN and bone marrow. *MS4a4C*, *MS4a6D* and *MS4a7* were expressed in all tissues examined. *MS4a8B* transcripts were expressed by spleen, peripheral lymph nodes, colon, liver, heart, lung and bone marrow. *MS4a10* transcripts were found in  
5 thymus, kidney, colon, brain, and testis. In addition, CD20 (*MS4a1*), FcεRIβ (*MS4a2*), and *MS4a3* expression were primarily restricted to hematopoietic tissues. *MS4a3*, *MS4a4B*, *MS4a4C*, *MS4a6B*, *MS4a6C*, *MS4a6D*, *MS4a7*, *MS4a8B*, and *MS4a10* were also expressed by various hematopoietic and lymphoblastoid cell lines. Therefore, most *MS4a* family members were  
10 expressed by hematopoietic cells.

Table 4

MS4a Gene Expression by Mouse Tissues<sup>a</sup>

MS4a	Thymus	Spleen	PLN	BM	Liver	Kidney	Heart	Colon	Lung	Brain	Teste
1	+	+++	+++	+	-	-	-	-	+	-	-
2	+	+	+	+++	-	+	-	-	+	-	-
3	+	+	+	+++	-	-	-	-	+	+	-
4B	+++	+++	+++	++	+	+	+	+	+	-	-
4C	+++	+++	+++	+++	+	+	+	+	+	+	+
4D	+	+	++	-	+	+	++	++	++	-	+
6B	+++	+++	+++	++	+	-	+	+	+	-	++
6C	+	+	+	++	-	-	-	-	-	-	-
6D	+++	+++	+++	++	+++	+++	+++	+++	+++	+++	+++
7	++	++	++	++	+	+	+	++	+	+	+
8B	-	+	+	+	+	-	+	++	+	-	-
10	+	-	-	-	-	+	-	+	-	+	++
G3PDH	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++

<sup>a</sup>Gene transcription was assessed by PCR amplification of cDNA generated from mRNA isolated from tissue samples. Values represent the level of  
15 PCR product generated relative to the glyceraldehyde-3-phosphate dehydrogenase (G3PDH) control as described for Table 3. Peripheral lymph node (PLN) and bone marrow (BM).

Expression of MS4A family members was also assessed in mouse hematopoietic cell lines (Table 5). Nine of the twelve MS4A genes were expressed in pre-B cell lines and five of the MS4A genes were expressed in B cell lines. Six of the MS4A genes were expressed by T cell lines. These data suggest that B cells can express most members of the MS4A gene family, although the patterns of expression of each gene is distinct.

Table 5

MS4a Expression by Mouse Lymphoid Tissues and Cell Lines<sup>a</sup>

	<u>Tissues</u>		<u>Pre B cell lines</u>			<u>B cell lines</u>		<u>T cell lines</u>	
MS4a	Spleen	Thymus	300.19	38B9	70Z	A20	AJ9	BW514	EL-14
1	+++	+	-	-	-	+++	+++	-	-
2	+	+	-	-	+	-	-	-	-
3	+	+	-	+	-	-	-	-	-
4B	+++	+++	-	-	-	-	-	-	++
4C	+++	+++	-	+	+	++	-	-	+
4D	+	+	-	-	-	-	-	-	-
6B	+++	+++	-	+	+++	+	-	+++	+++
6C	+	-	-	+	+	-	-	-	+
6D	+++	+++	-	++	+++	-	+	-	+++
7	++	++	-	-	++	-	-	-	-
8B	+	-	-	-	++	-	-	-	-
10	-	+	-	-	+	+	+	+	-
G3PDH	+++	+++	+++	+++	+++	+++	+++	+++	+++

10

<sup>a</sup>Gene transcription was assessed by PCR amplification of cDNA generated from mRNA isolated from each cell type. Values represent the level of PCR product generated relative to the glyceraldehyde-3-phosphate dehydrogenase (G3PDH) control in three separate PCR reactions: -, no specific PCR product detected; +, low levels of the appropriate band were detectable; ++ to +++, appropriate bands of increasing intensity were readily visualized in all samples examined. Identical results were obtained using two different primer pairs for cDNA amplification.

15

### III.B. Detection of MS4A Polymorphisms

In another embodiment, genetic assays based on nucleic acid molecules of the present invention can be used to screen for genetic variants by a number of PCR-based techniques, including single-strand conformation polymorphism (SSCP) analysis (Orita, M., et al. (1989) *Proc Natl Acad Sci USA* 86(8):2766-2770), SSCP/heteroduplex analysis, enzyme mismatch cleavage, and direct sequence analysis of amplified exons (Kestila et al. (1998) *Mol Cell* 1(4):575-582; Yuan et al. (1999) *Hum Mutat* 14(5):440-446). Automated methods can also be applied to large-scale characterization of single nucleotide polymorphisms (Brookes (1999) *Gene* 234(2):177-186; Wang et al. (1998) *Science* 280(5366):1077-82). The present invention further provides assays to detect a mutation of a variant MS4A locus by methods such as allele-specific hybridization (Stoneking et al. (1991) *Am J Hum Genet* 48(2):370-82), or restriction analysis of amplified genomic DNA containing the specific mutation.

### IV. Recombinant Production of a MS4A Polypeptide

The present invention also provides a method for recombinant production of a MS4A polypeptide, as described in Example 3. Preferably, the recombinant polypeptide comprises some or all of the amino acid sequences of any one of the even-numbered SEQ ID NOs:2-38.

Recombinantly produced proteins are useful for a variety of purposes, including structural determination of a MS4A polypeptide, generation of an antibody that recognizes a MS4A polypeptide, and screening assays to identify a chemical compound or peptide that interacts with a MS4A polypeptide, described further herein below.

### V. Production of MS4A Antibodies

In another aspect, the present invention provides a method of producing an antibody immunoreactive with a MS4A polypeptide, the method comprising recombinantly or synthetically producing a MS4A polypeptide, or portion thereof, to be used as an antigen. The MS4A

polypeptide is formulated so that it is can be used as an effective immunogen. An animal is immunized with the formulated MS4A polypeptide, generating an immune response in the animal. The immune response is characterized by the production of antibodies that can be collected from the blood serum of the animal. Optionally, cells producing a MS4A antibody can be fused with myeloma cells, whereby a monoclonal antibody can be selected. Exemplary methods for producing a monoclonal antibody that recognizes a MS4A protein are described in Example 4. Preferred embodiments of the method use a polypeptide set forth as any one of the even-numbered SEQ ID NOs:2-38.

The present invention also encompasses antibodies and cell lines that produce monoclonal antibodies as described herein.

The foregoing antibodies can be used in methods known in the art relating to the localization and activity of the MS4A polypeptide sequences of the invention, e.g., for cloning of MS4A nucleic acids, immunopurification of MS4A polypeptides, imaging MS4A polypeptides in a biological sample, measuring levels thereof in appropriate biological samples, and in diagnostic methods.

## 20 VI. Methods for Detecting a MS4A Polypeptide

In another aspect of the invention, a method is provided for detecting a level of MS4A polypeptide using an antibody that specifically recognizes a MS4A polypeptide, or portion thereof. In a preferred embodiment, biological samples from an experimental subject and a control subject are obtained, and MS4A polypeptide is detected in each sample by immunochemical reaction with the MS4A antibody. More preferably, the antibody recognizes amino acids of any one of the even-numbered SEQ ID NOs:2-38, and is prepared according to a method of the present invention for producing such an antibody.

30 In one embodiment, a MS4A antibody is used to screen a biological sample for the presence of a MS4A polypeptide. A biological sample to be screened can be a biological fluid such as extracellular or intracellular fluid,



or a cell or tissue extract or homogenate. A biological sample can also be an isolated cell (e.g., in culture) or a collection of cells such as in a tissue sample or histology sample. A tissue sample can be suspended in a liquid medium or fixed onto a solid support such as a microscope slide. In accordance with a screening assay method, a biological sample is exposed to an antibody immunoreactive with a MS4A polypeptide whose presence is being assayed, and the formation of antibody-polypeptide complexes is detected. Techniques for detecting such antibody-antigen conjugates or complexes are well known in the art and include but are not limited to centrifugation, affinity chromatography and the like, and binding of a labeled secondary antibody to the antibody-candidate receptor complex.

In one embodiment, an antibody that specifically recognizes a MS4A polypeptide can be used to assess the tissue- or cell-distribution of MS4A protein, for example, to evaluate CD20 expression during B lymphocyte development (Figure 9). CD20 expression in B220<sup>+</sup> lymphocytes from lymphoid tissues of wild type mice was examined by two-color immunofluorescence. In bone marrow, three types of B220<sup>+</sup> cells were detected. The vast majority of B220<sup>hi</sup> lymphocytes expressed CD20. However, the majority of B220<sup>lo</sup> lymphocytes were CD20-negative. Thus, CD20 was predominantly expressed by mature B cells.

CD19 expression is restricted to normal and neoplastic B cells and follicular dendritic cells. CD19 is expressed early by B progenitor cells in the bone marrow, presumably at the late pro-B or early pre-B cell stages around the time of immunoglobulin heavy chain rearrangement (Anderson et al. (1984) *Blood* 63:1424). Expression persists during all stages of B cell maturation and is lost upon terminal differentiation to plasma cells.

Double staining of CD20 with IgM and CD19 antibodies showed that some of the CD19<sup>lo</sup> and IgM<sup>lo</sup> cells were CD20 negative in the bone marrow. A few IgM- cells also expressed low levels of CD20 in the bone marrow. This data suggested that the CD20 expression was later than the CD19 expression but before or around the time of IgM expression during B cell

development in the bone marrow since these cells were gated on lymphocytes not dendritic cells.

The level of CD20 expression observed on mature B220<sup>hi</sup> B cells in bone marrow was maintained by B cells from peripheral lymphoid tissues.

5 The vast majority of B220<sup>+</sup> B cells in the spleen, blood, peripheral lymph nodes, and peritoneal cavity expressed CD20. Therefore, like human CD20, mouse CD20 was also exclusively expressed on B cells from the immature B cell stage to mature B cells.

10 VII. Identification of MS4A Modulators

VII.A. Screening for Small Molecule Ligands that Interact with a MS4A Polypeptide

The present invention further discloses a method for identifying a compound that modulates MS4A function. According to the method, a

15 MS4A polypeptide is exposed to a plurality of compounds, and binding of a compound to the isolated MS4A polypeptide is assayed. A compound is selected that demonstrates specific binding to the isolated MS4A polypeptide. Preferably, the MS4A polypeptide used in the binding assay of the method includes some or all amino acids of any one of the even-

20 numbered SEQ ID NOs:2-38.

Several techniques can be used to detect interactions between a protein and a chemical ligand without employing an *in vivo* ligand. Representative methods include, but are not limited to, Fluorescence Correlation Spectroscopy, Surface-Enhanced Laser Desorption/Ionization

25 Time-Of-flight Spectroscopy, and Biacore technology, as described in Example 5. These methods are amenable to automated, high-throughput screening.

Candidate regulators include but are not limited to proteins, peptides, and chemical compounds. Structural analysis of these selectants can

30 provide information about ligand-target molecule interactions that enable the development of pharmaceuticals based on these lead structures.

Similarly, the knowledge of the structure a native MS4A polypeptide provides an approach for rational drug design. The structure of a MS4A polypeptide can be determined by X-ray crystallography or by computational algorithms that generate three-dimensional representations. See Huang et al. (2000) *Pac Symp Biocomput* 230-41; Saqi et al. (1999) *Bioinformatics* 15:521-522. Computer models can further predict binding of a protein structure to various substrate molecules, that can be synthesized and tested. Additional drug design techniques are described in U.S. Patent Nos. 5,834,228 and 5,872,011.

10        VII.B. Methods for Identifying Modulators of MS4A Gene Expression

The assembly and annotation of genomic sequences comprising MS4A genes in the region of human chromosome 11q12-13.1, disclosed herein for the first time, identify MS4A gene regulatory regions. Preferably, MS4A gene regulatory regions comprise sequences upstream of the initial  
15        coding region of each MS4A gene as disclosed in SEQ ID NOs:73-81. An expression cassette comprising a MS4A promoter region can be employed in assays for the identification of modulators of MS4A expression. Thus the present invention also provides a method for identifying a substance that regulates MS4A gene expression using a chimeric gene that includes an  
20        isolated MS4A gene promoter region operably linked to a reporter gene. According to this method, a gene expression system is established that includes the chimeric gene and components required for gene transcription and translation so that reporter gene expression is assayable. To select a substance that regulates MS4A gene expression, the method further  
25        provides the steps of using the gene expression system to determine a baseline level of reporter gene expression in the absence of a candidate regulator; providing one or more candidate regulators to the gene expression system; and assaying a level of reporter gene expression in the presence of a candidate regulator. A candidate regulator is selected whose presence  
30        results in an altered level of reporter gene expression when compared to the baseline level.

Several molecular cloning strategies can be used to identify

substances that specifically bind a MS4A gene cis-regulatory element. In one embodiment, a cDNA library in an expression vector, such as the lambda-gt11 vector, can be screened for cDNA clones that encode a MS4A gene regulatory element DNA-binding activity by probing the library with a  
5 labeled MS4A DNA fragment, or synthetic oligonucleotide (Singh et al. (1989) *Biotechniques* 7:252-261). Preferably, the nucleotide sequence selected as a probe has already been demonstrated as a protein binding site using a protein-DNA binding assay, as described in Example 9.

In another embodiment, transcriptional regulatory proteins are  
10 identified using the yeast one-hybrid system (Luo et al. (1996) *Biotechniques* 20(4):564-568; Vidal et al. (1996) *Proc Natl Acad Sci USA* 93(19):10315-10320; Li & Herskowitz (1993) *Science* 262:1870-1874). In this case, a cis-regulatory element of a MS4A gene is operably fused as an upstream activating sequence (UAS) to one, or typically more, yeast reporter genes  
15 such as the *lacZ* gene, the *URA3* gene, the *LEU2* gene, the *HIS3* gene, or the *LYS2* gene, and the reporter gene fusion construct(s) is inserted into an appropriate yeast host strain. It is expected that the reporter genes are not transcriptionally active in the engineered yeast host strain, for lack of a transcriptional activator protein to bind the UAS derived from the MS4A gene  
20 promoter region. The engineered yeast host strain is transformed with a library of cDNAs inserted in a yeast activation domain fusion protein expression vector, e.g. pGAD, where the coding regions of the cDNA inserts are fused to a functional yeast activation domain coding segment, such as those derived from the GAL4 or VP16 activators. Transformed yeast cells  
25 that acquire a cDNA encoding a protein that binds a cis-regulatory element of a MS4A gene can be identified based on the concerted activation the reporter genes, either by genetic selection for prototrophy (e.g. *LEU2*, *HIS3*, or *LYS2* reporters) or by screening with chromogenic substrates (e.g., a *lacZ* reporter) by methods known in the art.

30 The present invention also provides an *in vivo* assay for discovery of modulators of MS4A gene expression. In this case, a transgenic non-human animal is made such that a transgene comprising a MS4A gene promoter

and a reporter gene is expressed and a level of reporter gene expression is assayable. Such transgenic animals can be used for the identification of compounds that are effective in modulating MS4A gene expression.

*In vitro* or *in vivo* screening approaches can also survey more than one  
5 modulatable transcriptional regulatory sequence simultaneously.

### VIII. Animal Models

The present invention further pertains to an animal model of disorders associated with a MS4A nucleic acid or polypeptide, including but not limited  
10 to atopic disorders, abnormal target cell development, function, and  $\text{Ca}^{++}$  responses. Such a model can be prepared by several methods. Using a transgenic approach, knock-out, knock-in, or knock-down mutation of the MS4A gene can suppress MS4A function. The present invention also teaches that an animal model of a MS4A-related disorder can be prepared  
15 by immunizing an animal with a MS4A polypeptide. The resulting immune response in the animal comprises a production of antibodies that specifically bind a MS4A polypeptide, thereby disrupting its biological activity. A method is also provided for generating an animal model of a MS4A-related disorder by administering to an animal a compound that disrupts MS4A expression or  
20 function. Such a compound is discovered by methods disclosed herein.

#### VIII.A. Generation of CD20-Deficient Mice

CD20-deficient mice were generated by targeted disruption of the *CD20* gene in embryonic stem (ES) cells using homologous recombination, as described in Example 6. A targeting vector was generated that replaces  
25 exons encoding part of the second extracellular loop, the 4<sup>th</sup> transmembrane domain, and the large carboxyl-terminal cytoplasmic domain of CD20 with a neomycin resistant gene (Figure 10A-D). Appropriate gene targeting generates an aberrant CD20 protein truncated at amino acid position 157 and fused with an 88 amino acid protein encoded by the *Neo'* gene promoter  
30 sequence.

After DNA transfections, 6 of 115 Neo-resistant ES cell clones carried the targeted allele as determined by Southern blot analysis of EcoR V



digested genomic DNA using a 1.5 kb DNA probe (Figure 10D). Appropriate targeting was further verified in two clones by Southern analysis of ES cell DNA digested with BamH I (>12 kb fragment was reduced to a 6.5 kb band in targeted cells), Kpn I (7.2 kb became 5.5 kb), and Ssp I (5.6 kb became 5 7.0 kb) using the same probe. Cells of one ES cell clone were injected into blastocysts that were transferred into foster mothers. Highly chimeric male offspring (80-100% according to coat color) bred with C57BL/6 (B6) females transmitted the mutation to their progeny (Figure 10E). Mice homozygous for disruption of the *CD20* gene were obtained at the expected Mendelian 10 frequency by crossing heterozygous offspring.

Appropriate targeting of the *CD20* gene was further verified by PCR analysis of genomic DNA from homozygous offspring (Figure 10F). Wild type *CD20* mRNA was absent in *CD20*<sup>-/-</sup> mice as confirmed by PCR amplification of cDNA generated from splenocytes of *CD20*<sup>-/-</sup> mice (Figure 15 10G). *CD20*-deficient mice (*CD20*<sup>-/-</sup>) thrived and reproduced as well as their wild type littermates and did not present any obvious anatomical or morphological abnormalities during the first year of life.

Absence of cell surface *CD20* protein expression in *CD20*<sup>-/-</sup> mice was further verified by staining B220<sup>+</sup> splenocytes with murine anti-*CD20* 20 monoclonal antibodies. Hybridomas producing these antibodies were generated using splenocytes from *CD20*<sup>-/-</sup> mice that were immunized with *CD20*-GFP cDNA-transfected 300.19 cells. Ten hybridomas secreted antibodies reactive with 300.19 (Figure 10H) and CHO (Figure 10I) cells transfected with *CD20*-GFP cDNA, but not with untransfected CHO or 25 300.19 cells (Table 6). These antibodies also reacted with *CD20* epitopes expressed on the cell surface of B220<sup>+</sup> splenocytes from wild type mice, but not with splenocytes from *CD20*<sup>-/-</sup> mice (Figure 10J). Therefore, targeted mutation of the *CD20* gene abrogated cell surface *CD20* protein expression.

Table 6  
Anti-CD20 Monoclonal Antibodies Generated in CD20<sup>-/-</sup> Mice<sup>a</sup>

Ab Name	Clone Name	Isotype	Whole Cell ELISA <sup>a</sup>		FACS Analysis <sup>b</sup>		
			CD20-CHO	CHO	CD20-300.19	300.19	Spleen
MB20-1	MCD20-5	IgG1, K	+	-	+	-	+
MB20-2	MCD20-61	IgG1, K	+	-	+	-	++
MB20-3	MCD20-86	IgG3, K	+	-	+	-	++
MB20-6	MCD20-223	IgG2a, K	+	-	+	-	+
MB20-7	MCD20-243	IgG2b, K	+	-	+	-	+
MB20-8	MCD20-270	IgG2b, K	+	-	+	-	+
MB20-10	MCD20-388	IgG2b, K	+	-	+	-	+
MB20-11	MCD20-392	IgG2a, K	+	-	+	-	+
MB20-13	MCD20-624	IgG3, K	+	-	+	-	++
MB20-14	MCD20-642	IgG1, K	+	-	+	-	++

<sup>a</sup>Values represent reactivity of the monoclonal antibody with adherent  
5 monolayers of CHO cells either transfected or untransfected with CD20-GFP  
cDNA as assessed by a cell-based ELISA. The monoclonal antibodies did  
not react with GFP cDNA-transfected CHO cells.

<sup>b</sup>Cell surface reactivity of the monoclonal antibody with single cell  
suspensions of 300.19 cells either transfected or untransfected with CD20-  
10 GFP cDNA or spleen cells from wild type mice. Values represent relative  
indirect immunofluorescence staining intensity as assessed by flow  
cytometry and shown in figure 10H-J.

### VIII.B. B Cell Development and Function in CD20<sup>-/-</sup> Mice

CD20<sup>-/-</sup> mice did not show an obvious propensity for infections during their first year of life. They had normal frequencies of IgM<sup>-</sup> B220<sup>lo</sup> pro/pre-B cells, IgM<sup>+</sup> B220<sup>lo</sup> immature B cells and IgM<sup>+</sup> B220<sup>hi</sup> mature B cells in the bone marrow (Figure 11, Table 7). Overall, the number of circulating and spleen IgM<sup>+</sup> B220<sup>+</sup> B cells found in CD20<sup>-/-</sup> mice was increased compared with wild type littermates (Table 7). However, an immunohistochemical analysis of spleen tissue sections revealed a normal architecture and organization of the spleen. In the bone marrow, overall IgM expression was decreased on immature B cells, yet increased on mature B cells when compared with IgM levels expressed by comparable cells in wild type littermates. However, overall IgM expression by mature B220<sup>hi</sup> B cells in the blood, spleen and lymph nodes was slightly lower in CD20<sup>-/-</sup> mice (Figure 11B-D). There were no obvious differences in the size (light scatter properties) of CD20<sup>-/-</sup> B cells isolated from bone marrow, blood, lymph nodes or spleen when compared with B cells from wild type littermates. These data therefore suggest that CD20 plays a functional role in the development and tissue localization of B cells.

Table 7Frequencies and Numbers of B Lymphocytes in CD20<sup>-/-</sup> Mice

Tissue	Phenotype	Wild Type	CD20 <sup>-/-</sup>	Wild Type	CD20 <sup>-/-</sup>
		% of B Lymphocytes		B cell numbers (x10 <sup>-6</sup> )	
Bone Marrow	B220 <sup>lo</sup> IgM <sup>-</sup>	36 ± 2	34 ± 3		
	B220 <sup>lo</sup> IgM <sup>+</sup>	19 ± 2	13 ± 2*		
	B220 <sup>hi</sup> IgM <sup>+</sup>	14 ± 2	16 ± 4		
Blood <sup>d</sup>	B220 <sup>+</sup> IgM <sup>+</sup>	61 ± 2	60 ± 3	3.6 ± 0.5	3.9 ± 0.5
Spleen	B220 <sup>+</sup> IgM <sup>+</sup>	51 ± 6	53 ± 5	58 ± 12	76 ± 12
Lymph Nodes <sup>e</sup>	B220 <sup>+</sup> IgM <sup>+</sup>	26 ± 6	19 ± 2	1.2 ± 0.3	0.9 ± 0.3
Peritoneum	B220 <sup>+</sup> IgM <sup>+</sup>	70 ± 4	69 ± 5	2.4 ± 0.3	3.1 ± 0.3
	B220 <sup>lo</sup> CD5 <sup>+</sup>	44 ± 4	15 ± 5**	1.5 ± 0.2	0.7 ± 0.2
	B220 <sup>hi</sup> CD5 <sup>-</sup>	28 ± 2	59 ± 3**	1.0 ± 0.1	2.7 ± 0.1

5 <sup>a</sup>Values represent mean (± SEM) results obtained from seven 2-month-old of wild type controls and 10 CD20<sup>-/-</sup> mice. Numbers represent the percentage of lymphocytes (based on side and forward light scatter properties) expressing the indicated cell surface markers.

<sup>b</sup>B cell numbers were calculated based on the total number of cells harvested from the indicated tissues.

10 <sup>d</sup>The values indicate the number of cells/ml.

<sup>e</sup>Values represent results from peripheral lymph nodes pairs.

\*The percentage or number was significantly different than in wild-type, p < 0.05; \*\* p < 0.01.

Within the peritoneal cavity, the number of IgM<sup>+</sup> B220<sup>+</sup> B cells in CD20<sup>-/-</sup> mice was similar to that of wild-type littermates (Table 7, Figure 11E). However, there was a 4-fold decrease in the number of CD5<sup>+</sup> B220<sup>lo</sup> B1a cells, with a compensatory increase in the number of CD5<sup>-</sup> B220<sup>hi</sup> B2 cells. Therefore, CD20-deficiency predominantly affected the development or clonal expansion of the B1 subpopulation of B cells within the peritoneal cavity. Exemplary methods for quantitating B cell populations are described in Example 7.

#### VIII.C. Reduced [Ca<sup>++</sup>]<sub>i</sub> Responses in CD20<sup>-/-</sup> B Cells

10 The loss of CD20 significantly altered early B cell signaling responses, measured as described in Example 8. Splenic B220<sup>+</sup> B cells from CD20<sup>-/-</sup> mice generated substantially reduced [Ca<sup>++</sup>]<sub>i</sub> responses following surface IgM ligation when compared with wild type B cells. Decreased [Ca<sup>++</sup>]<sub>i</sub> responses in CD20<sup>-/-</sup> B cells were observed in response  
15 to both optimal (40 µg/ml, Figure 12A) and suboptimal concentrations (5 µg/ml) of anti-IgM antibodies. Although the kinetics of [Ca<sup>++</sup>]<sub>i</sub> responses in CD20<sup>-/-</sup> B cells was not altered, the magnitude of both the immediate [Ca<sup>++</sup>]<sub>i</sub> increase and the sustained increase observed at later time points were inhibited by loss of CD20 expression. More dramatic decreases in [Ca<sup>++</sup>]<sub>i</sub>  
20 responses (>50%) by CD20<sup>-/-</sup> B cells were observed in response to CD19 ligation with optimal concentrations (40 µg/ml) of antibody (Figure 12A). Reduced [Ca<sup>++</sup>]<sub>i</sub> responses following CD19 ligation on CD20<sup>-/-</sup> B cells were likely to result from differences in signaling capacity since Thapsigargin-induced (Figure 12A) and Ionomycin-induced [Ca<sup>++</sup>]<sub>i</sub> responses were higher  
25 in CD20<sup>-/-</sup> B cells than in wild type B cells. In addition, CD19 expression levels were not significantly different between CD20<sup>-/-</sup> and wild type B cells (Figure 12A).

Chelation of extracellular calcium with EGTA reduced the kinetics and magnitude of the immediate [Ca<sup>++</sup>]<sub>i</sub> increase observed following IgM



crosslinking (Figure 12A). However, the  $[Ca^{++}]_i$  increase observed at later time points was not substantially inhibited by EGTA treatment. Similar results were observed in CD20<sup>-/-</sup> B cells. By contrast, chelation of extracellular calcium with EGTA almost eliminated the  $[Ca^{++}]_i$  response  
5 observed following CD19 crosslinking (Figure 12A). This suggests that transmembrane  $Ca^{++}$  flux contributes substantially to the  $[Ca^{++}]_i$  responses observed following CD19 crosslinking. That CD20-deficiency had a substantial effect on CD19-induced  $[Ca^{++}]_i$  responses suggests that CD20 can contribute significantly to transmembrane  $Ca^{++}$  flux.

10 The consequences of CD20 loss on transmembrane signal transduction was further evaluated by assessing total cellular protein tyrosine phosphorylation in purified B cells following IgM ligation. Although some variation was observed between B cells from individual mice in individual experiments, overall levels of tyrosine phosphorylation in resting  
15 splenic B cells were higher in CD20<sup>-/-</sup> B cells than in wild type mice (Figure 12C). In addition, protein phosphorylation in B cells from CD20<sup>-/-</sup> mice increased more significantly after B cell antigen receptor (BCR) ligation than in wild type B cells. Thus, while CD20 expression can influence BCR-induced tyrosine phosphorylation, decreased  $[Ca^{++}]_i$  responses in CD20<sup>-/-</sup> B  
20 cells are unlikely to result from significant abnormalities in transmembrane signaling through the BCR.

#### IX. Therapeutic Applications

Another aspect of the present invention is a therapeutic method  
25 comprising administering to a subject a substance that modulates MS4A biological activity. Therapeutic substances include but are not limited to chemical compounds, antibodies, and gene therapy vectors. Substances that are discovered by the methods disclosed herein are useful for therapeutic applications related to disorders of MS4A function.

In one embodiment, the present invention provides a method for disrupting MS4A function by immunizing a subject with an effective dose of the disclosed MS4A polypeptide. The immune system of the subject produces an antibody that specifically recognizes the MS4A polypeptide, and binding of the antibody to the MS4A polypeptide abolishes MS4A function.

In another embodiment, the present invention provides MS4A nucleic acid sequences and gene therapy methods for modulating MS4A activity in a target cell. The gene therapy vector can encode a MS4A or sequences encoding a nucleic acid molecule, peptide, or protein that interacts with a MS4A protein.

Vehicles for delivery of a gene therapy vector include but are not limited to a liposome, a cell, and a virus. Preferably, a cell is transformed or transfected with the DNA molecule or is derived from such a transformed or transfected cell. Alternatively, the vehicle is a virus, including a retroviral vector, adenoviral vector or vaccinia virus whose genome has been manipulated in alternative ways so as to render the virus non-pathogenic. Methods for creating such a viral mutation are detailed in U.S. Patent No. 4,769,331. Exemplary gene therapy methods are also described in U.S. Patent Nos. 5,279,833; 5,286,634; 5,399,346; 5,646,008; 5,651,964; 5,641,484; and 5,643,567.

The therapeutic methods of the present invention can be applied in the treatment of a variety of conditions, including in the treatment of non-Hodgkin's lymphoma and in the treatment of atopic disorders or other allergenic diseases. Application of the present inventive therapeutic methods are evidenced by the current U.S. Food and Drug Administration approved use of antibodies against CD20 in the treatment of non-Hodgkin's lymphoma. Additionally, the therapeutic methods of the present invention are illustrated in view of the recognition in the art that genetic variations at chromosome 11Q12-13 can also play a role in the pathogenesis of atopic disorders and other allergenic diseases. Indeed, it has been recognized that

FcεRIβ contributes to such diseases, and thus the MS4A genes identified in accordance with the present invention are envisioned also to contribute to allergenic disease. Therefore the present therapeutic methods, which pertain to the modulation of the biological activity of an MS4A polypeptide of the present invention have application with respect to the treatment of such disorders.

#### X. Summary

The invention comprises 19 new genes that are members of a class of genes encoding MS4A proteins. Three members have been described, CD20, FcεRIβ, and HTm4. A gene family has been defined based on a shared chromosomal location, conservation of protein size and structure, gene structure conservation, and similar expression in hematopoietic cells. MS4A proteins function as oligomeric cell surface complexes, and complex assembly using diverse MS4A members is implicated as a mechanism for regulating complex function.

Two members of this class, CD20 and FcεRIβ, have been described functionally, and in each case an important function has been delineated. CD20 is required for cell cycle progression and signal transduction in B lymphocytes. CD20 also regulates Ca<sup>++</sup> conductance, possibly as a cation channel subunit. Of clinical relevance, antibodies that recognize CD20 are effective in treating non-Hodgkin's lymphoma. FcεRIβ mediates interactions with IgE-bound antigens that lead to degranulation of mast cells, and variation of the FcεRIβ locus is implicated in allergenic disease.

The utility of the MS4A genes is based in part on overlapping or shared functions with known MS4A members. In one case, new MS4A genes have important potential as part of a CD20 complex. The structural description of CD20 complexes suggests that one or more CD20-related proteins constitute the functional complex. Thus, new MS4A proteins can define antigens useful for lymphoma treatment. In another case, MS4A

genes are implicated in IgE responses. Atopic disorders (allergy, asthma, eczema, allergic rhinitis) are dysfunctional IgE responses and are associated with a locus on human chromosome 11q containing most members of the MS4A gene family. FcεRIβ is one relevant factor, and recent work supports  
5 that FcεRIβ as well as other genetic elements in the region contribute to the disease. Thus, as disclosed herein, the present MS4A sequences also have utility in the characterization, diagnosis, and potential treatment of atopy linked to the chromosomal location wherein MS4A genes are located.

## 10 Examples

The following Examples have been included to illustrate modes of the invention. Certain aspects of the following Examples are described in terms of techniques and procedures found or contemplated by the present co-inventors to work well in the practice of the invention. These Examples  
15 illustrate standard laboratory practices of the co-inventors. In light of the present disclosure and the general level of skill in the art, those of skill will appreciate that the following Examples are intended to be exemplary only and that numerous changes, modifications, and alterations can be employed without departing from the scope of the invention.

## 20 Example 1

### Database Searches and cDNA Isolation

Three hundred and thirty seven nucleotide sequences obtained from the translated GenBank database of expressed sequence tags (ESTs) were assembled into sixty-two subgroups of contiguous linear segments based on  
25 their overlapping sequences and potential for encoding proteins homologous with CD20. Based on these subgroups, EST cDNAs (Figure 1) were obtained from the ATCC and sequenced. Based on the complete sequences of twenty-one near full-length EST cDNAs, eleven novel genes were defined in human and mouse that unified multiple EST subgroups.  
30 Near full-length EST clones representing these genes are shown in Figure 1.

These eleven genes and five additional genes were also identified by PCR amplification of transcripts using subgroup-specific primers or primers based on EST sequences. The specific details of how cDNAs representing the five genes that were not identified by EST cDNA clones are indicated below. In all cases, ESTs and cDNAs encoding the predicted coding regions of each putative unique gene were sequenced in both directions and at least two independent ESTs and/or cDNAs representing near full-length gene products were sequenced. Thereby, there was independent confirmation of accuracy for all of the sequences reported.

Based on EST subgroup sequences, cDNAs encoding mouse *MS4a4B* and *MS4a4C* were isolated by PCR amplification of C57BL/6 mouse spleen cDNA using both Taq and Pfu DNA polymerase. Primers for *MS4a4B* (SEQ ID NOs:63-64) amplified an 879 bp fragment. Primers for *MS4a4C* (SEQ ID NOs:65-66) amplified a 794 bp fragment. EST sequences for *MS4a4D* only encoded the 3' end of the predicted protein. Since *MS4a4D* sequences were closely related to *MS4a4B* and *MS4a4C* sequences, a sense 5' primer (SEQ ID NO:67) based on consensus *MS4a4B* and *MS4a4C* sequences and a *MS4a4D*-specific antisense primer (SEQ ID NO:68) were used to amplify a 773 bp fragment from cDNA of C57BL/6 mouse lung.

*MS4a6C* was initially identified based on one unique EST sequence (AA028258) encoding a mouse protein homologous with the C-terminal end of *MS4a6B*. *MS4a6C* cDNAs were isolated by PCR amplification of C57BL/6 mouse bone marrow cDNA using Taq polymerase. A primer based on identical sequences at the 5' end of the *MS4a6B* and *MS4a6D* cDNAs (SEQ ID NO:69) was used in combination with an antisense primer specific for the unique EST sequence (SEQ ID NO:70) to amplify a 787 bp fragment. Sequences from multiple independent PCR-amplified cDNAs were identical. Subsequently, the PCR-generated 5' end of the near full-length *MS4a6C* cDNA was found to be identical to an orphan EST subgroup sequence that had not been linked with defined 3' sequences. Thereby, the EST subgroup sequences verified that the PCR-amplified 5' end of the *MS4a6C* cDNAs



was appropriate. In addition, the overall *MS4a6C* sequence was similar to the sequence of *MS4a6B* cDNAs without interruption. Thus, the *MS4a6C* cDNA united sequences identical to those found in two non-overlapping CD20-homologous EST subgroups. cDNAs encoding a 473 bp fragment of mouse *MS4a3* were amplified from cDNA of C57BL/6 bone marrow as described above. Primers (SEQ ID NOs:71-72) were obtained based on a single thymic cDNA EST sequence (GenBank AA940479) where the corresponding cDNA was not available.

Human *MS4A* and mouse *MS4a* cDNA sequences (*MS4A1* to *MS4A12*) (disclosed herein) were used to search the htgs GenBank human genomic database of unfinished human genomic sequences (<http://www.ncbi.nlm.nih.gov/blast/>) using the BLAST program. Seventeen phase 1 or phase 2 human genomic DNA sequences encoding potential *MS4A* genes were assembled into groups of contiguous linear segments based on their overlapping sequences. Three EST clones corresponding to partial *MS4A6E* transcripts were obtained from the ATCC and sequenced completely on both DNA stands.

All PCR-amplified cDNAs were subcloned and sequenced entirely in both directions. Complete sequencing of at least two distinct PCR-generated cDNAs from both Taq and Pfu enzyme was performed in most cases. Differences between cDNA sequences were only noted when multiple cDNA clones generated by both Taq and Pfu polymerases revealed identical differences. In some cases, cDNAs or EST sequences contained potential intron|exon splice sites that delimited structural domains and aligned with the known intron|exon splice sites of CD20 (Tedder et al. (1989b) *J Immunol* 142:2560-2568). In these cases, potential introns were flanked by consensus splice donor and/or splice acceptor sequences (Aebi & Weissmann (1987) *Trends Genet* 3:102-107) or were likely to represent splice variants where exons were deleted.

## Example 2

### RNA Isolation and Reverse Transcription-PCR

Reverse transcription-PCR amplification (RT-PCR) was as described previously (Zhou & Tedder, 1995) with minor modifications. Total RNA was  
5 extracted from  $1-2 \times 10^7$  hematopoietic cell lines using a RNeasy Mini Kit (Qiagen, Inc., Chatsworth, California) according to the manufacturer's instructions. Human hematopoietic cell lines included one pre-B cell line (NALM-6), three B cell lines (BJAB, DAUDI, and SB), four T cell lines (HSB-2, HUT-78, JURKAT, and MOLT15), two myelomonocytic lines (HL60 and  
10 U937), and one erythroleukemia cell line (K562). RNA concentrations were determined by UV absorbance. Ten  $\mu\text{g}$  of total RNA was reverse transcribed. In some cases, cDNA from any of 8 different human tissues (colon, ovary, blood mononuclear cells, prostate, small intestine, spleen, testes, and thymus; from CLONETECH Laboratories, Inc., Palo Alto,  
15 California) was analyzed. RT-PCR amplification was performed using gene-specific primers identical with protein coding regions of the predicted MS4A genes during 35 cycles ( $94^\circ\text{C}$  for 1 min,  $55^\circ\text{C}$  for 1.5 min,  $72^\circ\text{C}$  for 1.5 min, followed by extension at  $72^\circ\text{C}$  for 5 min). Following amplification, the PCR products were separated on 1% agarose-ethidium bromide gels and  
20 photographed. G3PDH, a housekeeping gene, was also amplified to control for sample to sample variation. RNA amplified without reverse transcription was used as a negative control, and was negative in all cases.

## Example 3

### Recombinant Production of MS4A Protein

25 For recombinant production of a protein of the invention in a host organism, a nucleotide sequence encoding the protein is inserted into an expression cassette designed for the chosen host and introduced into the host where it is recombinantly produced. The choice of the specific regulatory sequences such as promoter, signal sequence, 5' and 3'  
30 untranslated sequence, and enhancer appropriate for the chosen host is within the level of ordinary skill in the art. The resultant molecule, containing

the individual elements linking in the proper reading frame, is inserted into a vector capable of being transformed into the host cell. Suitable expression vectors and methods for recombinant production of proteins are well known for host organisms such as *E. coli*, yeast, and insect cells (see, e.g.,  
5 Lucknow & Summers (1988) *Bio/Technol* 6:47). Additional suitable expression vectors are baculovirus expression vectors, e.g., those derived from the genome of *Autographica californica* nuclear polyhedrosis virus (AcMNPV).

Recombinantly produced proteins are isolated and purified using a  
10 variety of standard techniques. The actual techniques used varies depending upon the host organism used, whether the protein is designed for secretion, and other such factors. Such techniques are well known to the skilled artisan. See Ausubel et al. (1994).

#### Example 4

##### 15 Mouse Anti-Mouse CD20 Monoclonal Antibody Production

Hybridomas producing CD20-specific mouse monoclonal antibodies were generated by the fusion of NS-1 myeloma cells with spleen cells from a CD20<sup>-/-</sup> mouse immunized with a cell line expressing a mouse CD20-GFP fusion protein. The CD20-GFP fusion protein was generated by subcloning  
20 a fragment of the pmB1-1 cDNA (from 159 to 1050 bp of SEQ ID NO:39) into the PEGFP-N1 vector (Clontech Laboratories Inc., Palo Alto, California) to generate an open reading frame encoding the entire CD20 protein with GFP fused to the carboxyl-terminal end. The resulting plasmid was linearized with ApaL I and used to transfect 300.19 cells, a mouse pre-B cell line, and  
25 Chinese Hamster Ovary (CHO) cells. Transfection was by Lipofectamine following the manufacturer's instructions (Clontech Laboratories, Inc.). Transfected cells were selected using GENETICIN™ (1 mg/ml, GIBCOBRL) in RPMI 1640 media (Sigma) for 300.19 cells or H-12 nutrient mixture (GIBCOBRL) for CHO cells. Both media were supplemented with 10% FCS,  
30 L-glutamine, streptomycin and penicillin. Transfected cells expressing high levels of CD20-GFP were isolated by fluorescence-based cell sorting.

### Example 5

#### *In vitro* Binding Assays

Recombinant protein can be obtained, for example, according to the approach described in Example 4 herein above. The protein is immobilized  
5 on chips appropriate for ligand binding assays. The protein immobilized on the chip is exposed to sample compound in solution according to methods well known in the art. While the sample compound is in contact with the immobilized protein, measurements capable of detecting protein-ligand interactions are conducted. Measurement techniques include, but are not  
10 limited to, SEDLI, Biacore, and FCS, as described above. Compounds found to bind the protein are readily discovered in this approach and are subjected to further characterization.

### Example 6

#### Generation of CD20-Deficient Mice

15 DNA encoding the *CD20* gene was isolated from a phage library prepared from 129/Sv strain mouse DNA (Figure 10A), mapped with restriction endonucleases, and sequenced to identify intron|exon boundaries (Figure 10B). The targeting vector was constructed using a pBluescript SK (Stratagene, La Jolla, California)-based targeting vector (p594, provided by  
20 Dr. David Milstone, Brigham and Women's Hospital, Boston, Massachusetts). A DNA fragment starting at the Pst I site in *CD20* exon 5 through the EcoR V site in exon 6 (~1.8 kb) was isolated and blunt end ligated into the targeting vector downstream of the pMC1-HSV thymidine kinase gene and upstream of the neomycin resistance marker obtained from  
25 pGK-neo poly A (Stratagene) that contained the PGK promoter and poly A signal sequence. An ~10 kb DNA fragment beginning at the Kpn I site downstream of exon 8 was also isolated and inserted into the targeting vector downstream of the neomycin resistant gene. The plasmid was linearized using a unique Sal I restriction site proximal to the 3' end of the  
30 *CD20* gene insert and used to transfect ES cells.

ES cells were transfected with linearized plasmid DNA and selected for G418 resistance as described (Keller and Smithies (1989) *Proc Natl Acad Sci USA* 86:8932). Genomic DNA from individual selected clones was digested with EcoR V and used for Southern blot analysis along with a  
5 radiolabeled ~1.5 kb DNA probe that was external to the targeting vector (Figure 10D). A 4.6 kb genomic DNA fragment hybridized with the probe in wild type ES cells or a 6.3 kb fragment in appropriately targeted ES cells (Fig 1E). Genomic DNA generated by BamH I, Ssc I or Kpn I digestion was also analyzed for appropriate targeting. The Southern blot pattern obtained in all  
10 cases was consistent with the appropriate predicted mutation indicating that detrimental recombinations did not occur in the vicinity of the desired homologous recombination. Cells from appropriately targeted ES cell clones were injected into 3.5 day old C57BL/6 blastocysts that were transferred into foster mothers. Offspring carrying the mutant CD20 allele were identified by  
15 Southern blot analysis of DNA obtained from tail biopsies.

High chimeric males (80-100% according to color) were bred with C57BL/6 (B6) females to generate heterozygous offspring with germline gene transmission, which were crossed to generate the homozygous CD20<sup>-/-</sup> and wild type littermates used for this study. In some cases, B6/129F1J  
20 (Jackson Laboratory) were used as controls. Results obtained using wild type littermates of CD20<sup>+/-</sup> mice were similar and were therefore pooled. All mice were between 2-3 months of age when used for this study. Mice were housed in a specific pathogen-free barrier-facility. All studies and procedures were approved by the Animal Care and Use Committee of Duke  
25 University.

### Example 7

#### Flow Cytometric Analysis of Lymphocyte Subsets

Single cell suspensions of lymphocytes from the spleen, bone marrow, peripheral lymph nodes, and peritoneal cavity were isolated from  
30 CD20<sup>-/-</sup> and wild type mice and counted using a hemocytometer prior to two-color immunofluorescence analysis. Retroorbital venous plexus puncture



was utilized to obtain circulating leukocytes. Leukocytes ( $0.5 \times 10^6$ ) were stained at 4°C using predetermined optimal concentrations of the test monoclonal antibody for 20 min as described (Zhou et al. (1994) *Mol Cell Biol* 14:3884-3894). Blood erythrocytes were lysed after staining using the  
5 Coulter Whole Blood Immuno-Lyse kit as detailed by the manufacturer (Coulter, Inc., Miami, Florida). Cells were washed and analyzed on a FACScan flow cytometer (Becton Dickinson, San Jose, California).

Antibodies used in this study included the following: biotin, FITC-conjugated anti-B220 Mab (CD45RA, RA-3, 6B2, provided by Dr. Robert  
10 Coffman, DNAXCORP, Palo, Alto, California); PE-conjugated anti-mouse Thy1.2 (Caltag Laboratories, Burlingame, California); B220-PE (Caltag Laboratories, Burlingame, California); biotin-conjugated anti-I-A (BD PharMingen, Franklin Lakes, New Jersey); PE or APC-conjugated anti-CD5 (BD PharMingen); PE-conjugated goat anti-mouse IgG3-specific antibody  
15 (Southern Biotechnology Associates Inc., Birmingham, Alabama); and biotin-conjugated anti-mouse IgD (Southern Biotechnology Associates Inc., Birmingham, Alabama). FITC or biotin-conjugated goat anti-mouse IgM isotype-specific antibodies (Southern Biotechnology Associates Inc., Birmingham, Alabama) were also used.

20 Phycoerythrin-conjugated Streptavidin (Southern Biotechnology Associates Inc., Birmingham, Alabama) was used to reveal biotin-coupled monoclonal antibody staining. The percent positively stained lymphocytes was determined using a FACScan flow cytometer (Becton Dickinson, San Jose, California). Positive and negative populations of cells were  
25 determined by using unreactive monoclonal antibody (Caltag Laboratories, Burlingame, California) as controls for background staining. Background levels of staining were delineated using gates positioned to include 98% of the control cells. Ten thousand cells with the forward and side light scatter properties of lymphocytes were analyzed for each sample.

### Example 8

#### Intracellular Calcium Measurements

Changes in lymphocyte  $[Ca^{2+}]_i$  levels were monitored by flow cytometry analysis as described (Fujimoto et al. (1999) *Immunity* 11:191).

5 Single cell suspension of splenocytes were resuspended ( $1 \times 10^7$ /ml) in RPMI 1640 medium containing 5% FBS, 10 mM HEPES and loaded with  $1\mu M$  of indo-1-AM for 30 min at  $37^\circ C$ . Splenocytes were then washed and incubated with a predetermined optimal concentration of FITC-conjugated anti-B220 monoclonal antibody for 15 min at room temperature. The

10 splenocytes were washed again and resuspended at  $2 \times 10^6$ /ml in medium. The fluorescence ratio (405/525 nm) of B220<sup>+</sup> splenic B cells was monitored by flow cytometry at baseline for 1 min and for 6 min after stimulation with optimal and suboptimal concentrations of goat F(ab')<sub>2</sub> anti-IgM antibody (5-40  $\mu g$ /ml), optimal concentrations of anti-mouse CD19 monoclonal antibody

15 (40  $\mu g$ /ml), Thapsigargin (1  $\mu g$ /ml; Sigma), or Ionomycin (2.67  $\mu g$ /ml; Calbiochem Biosciences, Inc., La Jolla, California). In some cases, EGTA (5 mM final; pH 7.0) was added to the cells, immediately followed by stimulation with the inducing agents described above. Results were plotted as the fluorescence ratio at 20 sec intervals with background fluorescence

20 subtracted. An increase in the fluorescence ratio indicates an increase in  $[Ca^{2+}]_i$ .

### Example 9

#### Characterization of a MS4A Promoter Region

A preferred *in vitro* technique for evaluating MS4A promoter function

25 is a transient transfection assay. According to this method, one or more chimeric reporter genes comprising a MS4A promoter region is introduced into a relevant host cell (e.g., a hematopoietic cell), and the resulting level of reporter gene expression is quantitated. Representative methods for making an expression system comprising a promoter region operably linked to a

30 heterologous reporter sequence are disclosed in U.S. Patent No. 6,087,111.

To analyze the function of a MS4A promoter region *in vivo*, transgenic

mice bearing a chimeric gene comprising a MS4A promoter region are generated, and a level of reporter gene expression in each mouse is determined.

5        Within a candidate promoter region or response element, the presence of regulatory proteins bound to a nucleic acid sequence can be detected using a variety of methods well known to those skilled in the art (Ausubel et al., 1992). Briefly, *in vivo* footprinting assays demonstrate protection of DNA sequences from chemical and enzymatic modification within living or permeabilized cells. Similarly, *in vitro* footprinting assays  
10   show protection of DNA sequences from chemical or enzymatic modification using protein extracts. Nitrocellulose filter-binding assays and gel electrophoresis mobility shift assays (EMSAs) track the presence of radiolabeled regulatory DNA elements based on provision of candidate transcription factors. Computer analysis programs, for example TFSEARCH  
15   version 1.3 (Yutaka Akiyama: "TFSEARCH: Searching Transcription Factor Binding Sites", <http://www.rwcp.or.jp/papia/>), can also be used to locate consensus sequences of known cis-regulatory elements within a genomic region.

### References

The publications and other materials listed below and/or set forth in the text above to illuminate the background of the invention, and in particular cases, to provide additional details respecting the practice, are incorporated  
5 herein by reference. Materials used herein include but are not limited to the following listed references.

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It will be understood that various details of the invention can be changed without departing from the scope of the invention. Furthermore, the foregoing description is for the purpose of illustration only, and not for the purpose of limitation--the invention being defined by the claims.

20

CLAIMS

What is claimed is:

1. An isolated MS4A polypeptide, or functional portion thereof, comprising:

- 5 (a) a polypeptide encoded by the nucleotide sequence of any one of the odd-numbered SEQ ID NOs:1-37;
- (b) a polypeptide encoded by a nucleic acid molecule that is substantially identical to any one of the odd-numbered SEQ ID NOs:1-37;
- 10 (c) a polypeptide having the amino acid sequence of any one of the even-numbered SEQ ID NOs:2-38;
- (d) a polypeptide that is a biological equivalent of the polypeptide of any one the even-numbered SEQ ID NOs:2-38; or
- 15 (e) a polypeptide which is immunologically cross-reactive with an antibody that shows specific binding with a polypeptide of any one of the even-numbered SEQ ID NOs:2-38.

2. An isolated nucleic acid molecule encoding a MS4A polypeptide, comprising:

20

- (a) the nucleotide sequence of any one of the odd-numbered SEQ ID NOs:1-37; or
- (b) a nucleic acid molecule substantially identical to any one of the odd-numbered SEQ ID NOs:1-37.

25 3. The isolated nucleic acid molecule of claim 2, comprising a 20 nucleotide sequence that is identical to a contiguous 20 nucleotide sequence of any one of the odd-numbered SEQ ID NOs:1-37.

4. A chimeric gene, comprising the nucleic acid molecule of claim 2 operably linked to a heterologous promoter.

5. A vector comprising the chimeric gene of claim 4.
6. A host cell comprising the chimeric gene of claim 4.
7. The host cell of claim 6, wherein the cell is selected from the group consisting of a bacterial cell, a hamster cell, a mouse cell, and a human cell.
8. A method of detecting a nucleic acid molecule that encodes a MS4A polypeptide, the method comprising:
  - (a) procuring a biological sample comprising nucleic acid material;
  - 10 (b) hybridizing the nucleic acid molecule of claim 2 under stringent hybridization conditions to the biological sample of (a), thereby forming a duplex structure between the nucleic acid of claim 2 and a nucleic acid within the biological sample; and
  - 15 (c) detecting the duplex structure of (b), whereby a MS4A nucleic acid molecule is detected.
9. An antibody that specifically recognizes a MS4A polypeptide of claim 1.
10. A method for producing an antibody that specifically recognizes a MS4A polypeptide, the method comprising:
  - (a) recombinantly or synthetically producing a MS4A polypeptide, or portion thereof;
  - (b) formulating the polypeptide of (a) whereby it is an effective immunogen;
  - 25 (c) administering to an animal the formulation of (b) to generate an immune response in the animal comprising production of antibodies, wherein antibodies are present in the blood serum of the animal; and



- (d) collecting the blood serum from the animal of (c), the blood serum comprising antibodies that specifically recognize a MS4A polypeptide.

11. A method for detecting a level of MS4A polypeptide, the  
5 method comprising

- (a) obtaining a biological sample comprising peptidic material; and
- (b) detecting a MS4A polypeptide in the biological sample of (a) by immunochemical reaction with the antibody of  
10 claim 9, whereby an amount of MS4A polypeptide in a sample is determined.

12. A method for identifying a substance that modulates MS4A function, the method comprising:

- (a) isolating a MS4A polypeptide of claim 1;
- 15 (b) exposing the isolated MS4A polypeptide to a plurality of substances;
- (c) assaying binding of a substance to the isolated MS4A polypeptide; and
- 20 (d) selecting a substance that demonstrates specific binding to the isolated MS4A polypeptide.

13. A method for modulating MS4A function in a subject, the method comprising:

- (a) preparing a pharmaceutical composition, comprising a substance identified according to the method of claim 10  
25 or 12, and a carrier; and
- (b) administering an effective dose of the pharmaceutical composition to a subject, whereby MS4A activity is altered in the subject.

14. The method of claim 13, wherein the substance is an antibody, a protein, a peptide, or a chemical compound.

15. The method of claim 13, wherein MS4A activity is regulation of the abundance of target cell subpopulations.

5 16. The method of claim 13, wherein MS4A activity is regulation of  $[Ca^{2+}]_i$  levels.

17. A method for identifying a candidate compound as a modulator of MS4A gene expression, the method comprising:

10 (a) exposing a cell sample with a candidate compound to be tested, the cell sample containing at least one cell containing a DNA construct comprising a modulatable transcriptional regulatory sequence of a MS4A-encoding nucleic acid and a reporter gene which is capable of producing a detectable signal;

15 (b) evaluating an amount of signal produced in relation to a control sample; and

(c) identifying a candidate compound as a modulator of MS4A gene expression based on the amount of signal produced in relation to a control sample.

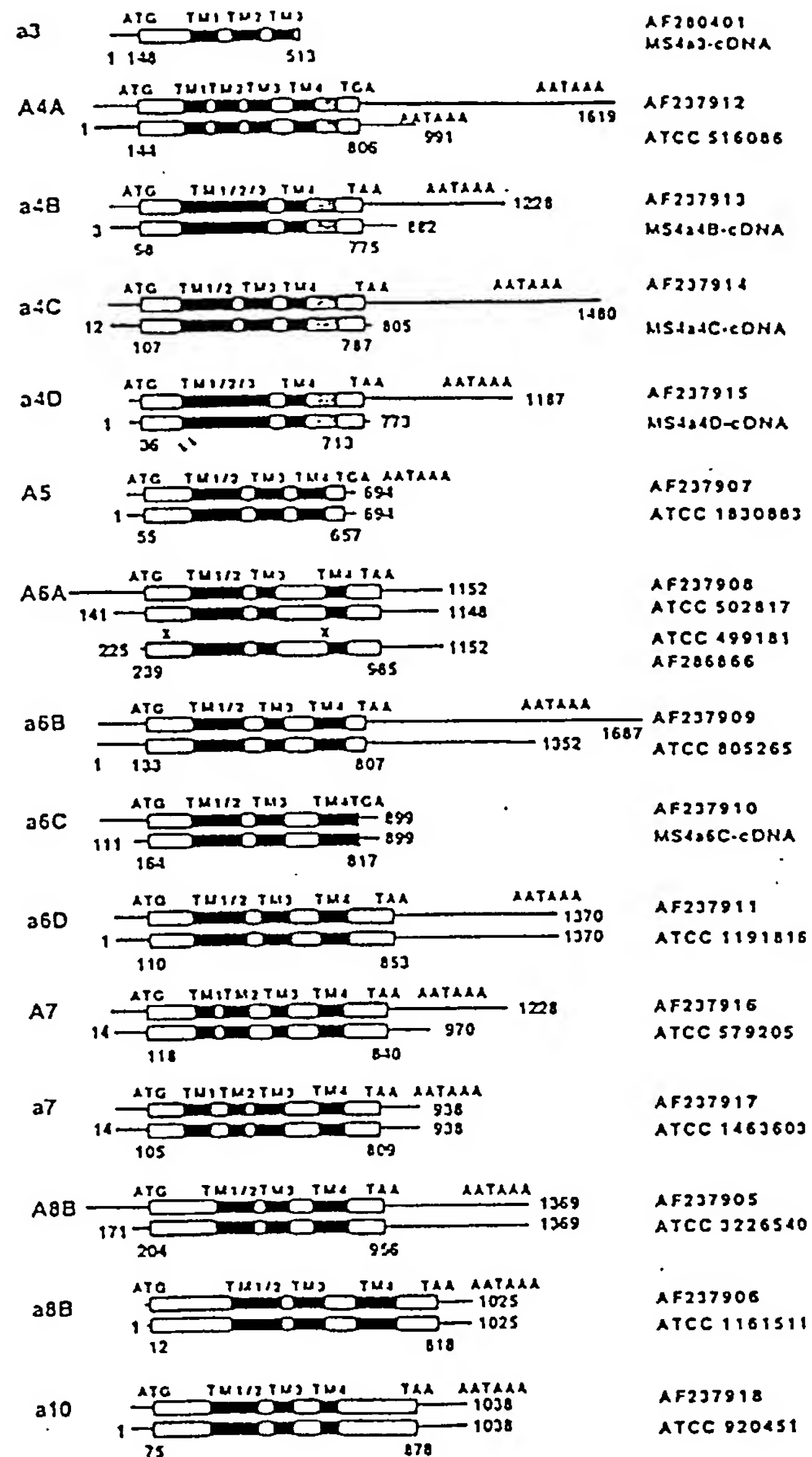
20 18. The method of claim 17, wherein the modulatable transcriptional regulatory sequence of a MS4A-encoding nucleic acid comprises a sequence that is immediately upstream of the initial coding region of a MS4A gene as set forth in any one of SEQ ID NOs:73-81.

25 19. A method for modulating MS4A function in a subject, the method comprising:

30 (a) preparing a gene therapy vector having a nucleotide sequence encoding a MS4A polypeptide or a nucleotide sequence encoding a nucleic acid molecule, peptide, or protein that interacts with a MS4A nucleic acid or polypeptide; and

- (b) administering the gene therapy vector to a subject, whereby the function of MS4A in the subject is modulated.

Figure 1



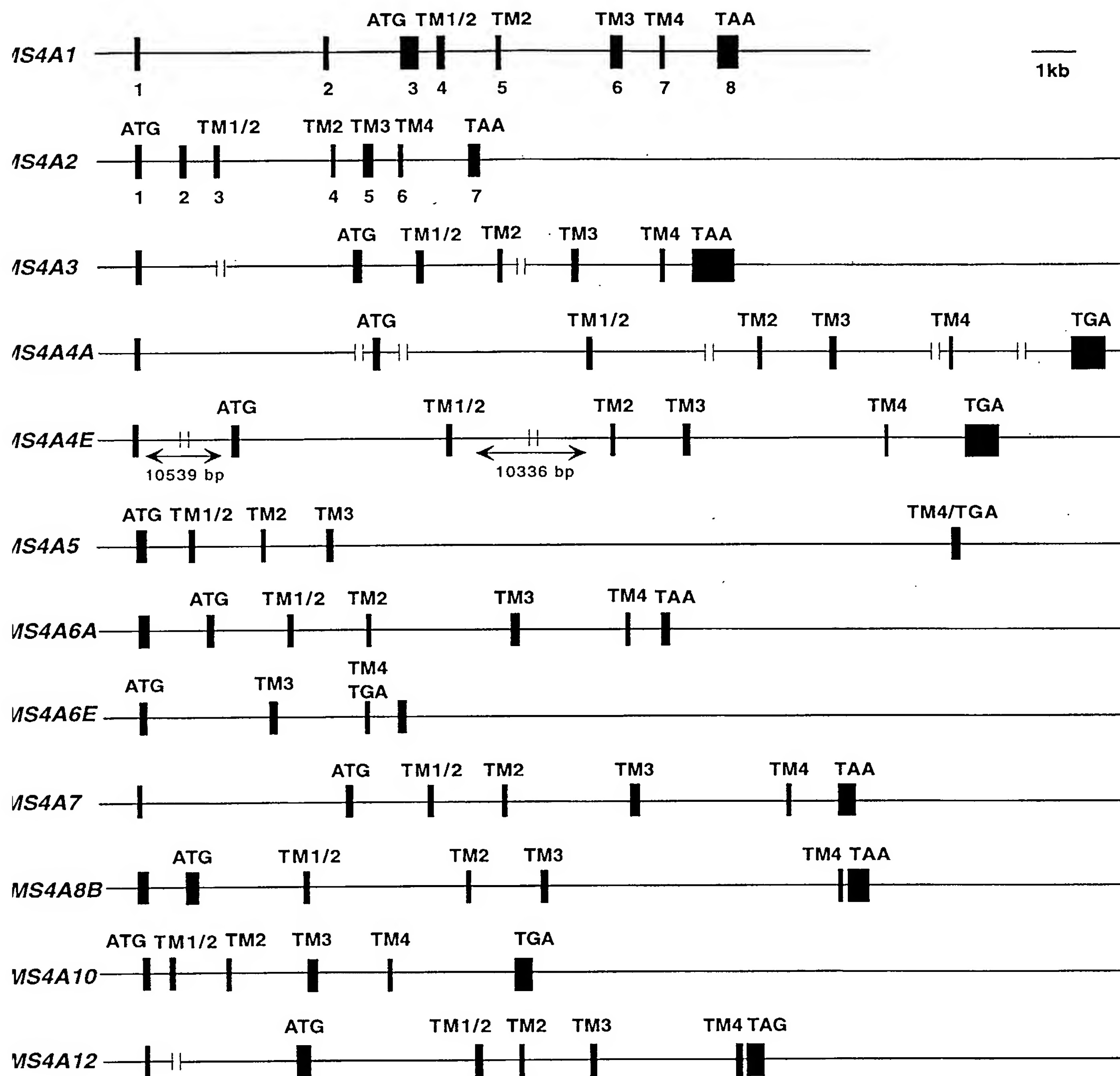


Figure 2



Figure 3

A4E ATGCGGAAA TG GGGGCT GTAGGAGAAT GGTGTCTGAG AGAAGACAGA AAC TGTTAGT  
 A4A ATGTGGGCAA TGGTGGGAA GTGGGGGAAT AGTGTCTGAG AGAAGATAGA GACTATAAAA TGCTGTTCAT

A4E GTGTGAGAAG ATTAGATGCT GTGGTGGGTT TGTGTCTATT CTTGTAAGGT GGTCAATGCC GGGGGAGTGG AAC 3  
 A4A GTGTGAGAAG ATTAGATGAT GTGGTGGGTT TGTGTCTATT CTTGTAAGGT GGTCA CA AGAGGGGTGG AAC 3

A4E ATT CCT GCA AAC GGG CTC AAC ATA TGC AAA TGT CTC AAT ATA GGA ATG AAA TTA CTT 60  
 A4A ATT CCT GCA AAT GGT TTC AAT ATA TGC AGA TGT CTC GAT ATA GGA ATG AAA TTA CGT CTT 63

A4E TAG AAC AAC TTA AAT AAG TCC AAT ATA CTT GGG GCT TTA AAA AAT AAA AAG GAG AAA TTC 120  
 A4A TGG AAC AAC TTA AAT AAG TCA AAT ATA CTT GGA GCT TTA AA AAT TAA AAG GAG AGA GAT 122

A4E M T T M Q G M E Q T T P G  
 A4E AAG AGC ACC TTT TCT GCT GCC ATG ACA ACC ATG CAA GGA ATG GAA CAG ACC ACT CCA GGG 180  
 A4A TCG AG C ACC TTT TCT GCT GCC ATG ACA ACC ATG CAA GGA ATG GAA CAG GCC ATG CCA GGG 182

A4E P G P D V P Q L G N I D V I H S Y L C K  
 A4E CCT GGC CCT GAT GTG CCC CAG CTG GGA AAC ATA GAT GTC ATA CAT TCA TAT CTG TGT AAA 240  
 A4A GCT GGC CCT GGT GTG CCC CAG CTG GGA AAC ATG GCT GTC ATA CAT TCA CAT CTG TGG AAA 142

A4E G L Q E K F F K R K P K V L G V V R I L  
 A4E GGA TTG CAA GAG AAG TTC TTC AAG AGG AAA CCC AAA GTC CTT GGG GTT GTG CGG ATT CTC 300  
 A4A GGA TTG CAA GAG AAG TTC TTG AAG GGA GAA CCC AAA GTC CTT GGG GTT GTG CAG ATT CTC 302

A4E I A L M S L S M G I I M M C V A F S S Y  
 A4E ATT GCC TTG ATG AGC CTT AGC ATG GGA ATA ATA ATG ATG TGT GTT GCA TTT AGT TCT TAT 360  
 A4A ACT GCC CTG ATG AGC CTT AGC ATG GGA ATA ACA ATG ATG TGT ATG GCA TCT AAT ACT TAT 362

A4E E E H P I F V Y V A Y T I W G S V M F I  
 A4E GAA GAA CAT CCC ATT TTT GTG TAT GTT GCG TAC ACA ATT TGG GGG TCA CTG ATG TTT ATT 420  
 A4A GGA AGT AAC CCT ATT TCC GTG TAT ATC GGG TAC ACA ATT TGG GGG TCA GTA ATG TTT ATT 422

A4E I S V S L S V A A G I R T T K G L V G G  
 A4E ATT TCA GTA TCC TTA TCA GTT GCA GCA GGA ATT AGA ACA AAA GGT CTG GTT GGA GGT 480  
 A4A ATT TCA GGA TCC TTG TCA ATT GCA GCA GGA ATT AGA ACT ACA AAA GGC CTG GTC CGA GGT 482

A4E S L G K N I T S S V L A I S G I L I N A  
 A4E AGT CTA GGA AAG AAT ATC ACC AGT TCA GTC TTG GCT ATA TCA GGG ATC TTA ATC AAT GCA 540  
 A4A AGT CTA GGA ATG AAT ATC ACC AGC TCT GTA CTG GCT GCA TCA GGG ATC TTA ATC AAC ACA 542

A4E I S L T F Y S F R Y H Y C N H D Q L S S  
 A4E ATA AGC TTG ACG TTT TAT TCA TTC CGT TAC CAT TAC TGT AAC CAC GAT CAG TTG TCA AGT 600  
 A4A TTT AGC TTG GCG TTT TAT TCA TTC CAT CAC CCT TAC TGT AAC TAC TAT GGC AAC TCA AAT 602

A4E N C Y M T M S I L M G T D G M V L L L S  
 A4E AAT TGT TAC ATG ACT ATG TCC ATT TTA ATG GGT ACG GAT GGC ATG GTG CTC CTC TTA AGT 660  
 A4A AAT TGT CAT GGG ACT ATG TCC ATC TTA ATG GGT CTG GAT GGC ATG GTG CTC CTC TTA AGT 662

A4E V L E F C I A V S L S A F G C K V L C C  
 A4E GTG CTG GAA TTC TGC ATT GCT GTG TCC CTC TCT GCC TTT GGA TGT AAA GTG CTT TGT TGT 720  
 A4A GTG CTG GAA TTC TGC ATT GCT GTG TCC CTC TCT GCC TTT GGA TGT AAA GTG CTC TGT TGT 722

A4E S P S E F V L I T P S N S H M A E I A S  
 A4E AGC CCC AGT GAG TTT GTG CTA ATT ACA CCA TCA AAT TCT CAC ATG GCA GAA ATA GCA TCT 780  
 A4A ACC CCT GGT GGG GTT GTG TTA ATT CTG CCA TCA CAT TCT CAC ATG GCA GAA ACA GCA TCT 782

A4E P T P L K T V \*  
 A4E CCC ACA CCA CTT AAG ACA GTT TGA TGCCACCAAA AGATTAACAG AAGAATGCTC CAGAAATCTA 844  
 A4A CCC ACA CCA CTT AAT GAG GTT TGA TGCCACCAAA AGATCAACAG ACAAATGCTC CAGAAATCTA 846

A4E TGCTGACTGT AACACAAGAA CC CACATGA GAAAGTACCA GAATCCAAT CCAATACTGA TAGACATATT 913  
 A4A TGCTGACTGT GACACAAGAG CCTCACATGA GAAATACCA GTATCCAAT TCGATACTGA TAGACTTGTT 916

A4E GATATCATTA TTATATGGAA TCCAATTATG ACCTCTGTGT GTGTGTGTGT GTGTATATAT ATATATACAT 983  
 A4A GATATTATTA TTATATGTAA TCCAATTATG AACTGTGTGT GTATA 961

A4E ATATATATAT ATACATATAT ATATATGTGT GTGTGTGTAT ATATTCAAAA TTTTGTCTC ATTTTTCCTC 1053  
 A4A GAGAGAT AAT AAA TTTCAAAA TTATGTCTC ATTTTTCCTC 1001

A4E CTGGAATCA ACAACTAATT TCATTGGCCC TTTATCGAGA GACTAGAAG TTAATTTAAT AAT AAATAATGCA 1123  
 A4A CTGGAATCA ATAACCTATT TCACTGGCTC TTTATCGAGA GACTAGAAG TTAATTTAAT AAT AAATAATGCA 1071

A4E TTTAATGAGG CAGCAGCACT TGAAAGGTTT TCATTTCATCA TTAGGACTTT ATATAAAGGC ATTAACTGGC 1194  
 A4A TTTAATGAGG CAACAGCACT TGAAAGGTTT TCATTTCATCA TAAGAACTTT ATATAAAGGC ATTACATTGGC 1142

A4E AAATAAGATT TGGAAACAGA AGGGCAAAA GGTATTG CTAACACGAG GTCTCCATGC AAA CACATA 1259  
 A4A AAATAAGATT TGGAAACAGA AGAGCAAAA AAAGATATTG TTAATAAGAG GCCTCCATGC AAAACACATA 1212

A4E CTTCTGCTCC CCTGTATAAC ATTCTCTCA CTTACTTGAC TTTTCTCTG CCATATTTGG GGACCAAAGT 1329  
 A4A CTTCC CTCC C ATTTAT TTA ACTT TTTTCTCTC CTACCTATGG GGACCAAAGT 1265

A4E GCTTTTCTCT TCATGAAGTG GAGATTCATG CCCTTCTCCC CCCTCTTTT CCTTCT GCTTCTCTTC 1395  
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A4E ACCCATAGAA AGTACCTTG AATAGTATAG TCAGTCCCTG CATGTGCACA AGCTATCATT TCAGTAAAGG 1465  
 A4A ACCCATAGAA AGTACCTTGA AGTAGCACAG TCCGTCTTG CATGTGCACG AGCTATCATT TGAGTAAAGG 1405

A4E TATACATGGA GTAAAAATCA TATGAAGGAT CAGATTCAAC TTATATTTTC TATTTTCTCT TCTTCTCTCTC 1535  
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A4E CCTTCCCCCA CCTTCTGCTG GGCAGAAATTA TATCTTAATC AAATGTGTAT CCTGTGTAC ATATGGAAAT 1605  
 A4A CCTTCTCCCC CCTTCTACTG GGCATAATTA TATCTTAATC ATATATGGAA ATGTGCAAC ATATGGTATT 1544

A4E GTGCAACATA TGCTATTTGT TAATGTTTGT TAATTACATT TGCTTTTATA TTGCAGAGCA AAATAAAAT 1675  
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A4E TAGAAG CAATACTTT ATCT 1695  
 A4A AAATTAGAG CAATAAAAAAA AAAAAA AAAA 1619

A6E								M	T	S	Q	P	I	S	N	E	T	I	I	M	
A6E			TT	GGC	AAC	ACC	ATT	ATG	ACA	TCA	CAA	CCT	ATT	TCC	AAT	GAG	ACC	ATC	ATA	ATG	53
A6A			TT	GGC	AAC	ACC	ATC	ATG	ACA	TCA	CAA	CCT	GTT	CCC	AAT	GAG	ACC	ATC	ATA	GTG	277
A6E	L	P	S	N	V	I	N	F	S	Q	A	E	K	P	E	P	T	N	Q	G	
A6E	CTC	CCA	TCA	AAT	GTC	ATC	AAC	TTC	TCC	CAA	GCA	GAG	AAA	CCC	GAA	CCC	ACC	AAC	CAG	GGG	113
A6A	CTC	CCA	TCA	AAT	GTC	ATC	AAC	TTC	TCC	CAA	GCA	GAG	AAA	CCC	GAA	CCC	ACC	AAC	CAG	GGG	337
A6E	Q	D	S	L	K	K	R	L	Q	A	K	V	K	V	I	G					
A6E	CAG	GAT	AGC	CTG	AAG	AAA	CGT	CTA	CAG	GCA	AAA	GTC	AAA	<u>GTT</u>	<u>ATT</u>	<u>GGG</u>					161
A6A	CAG	GAT	AGC	CTG	AAG	AAA	CAT	CTA	CAC	GCA	GAA	ATT	AAA	<u>GTT</u>	<u>ATT</u>	<u>GGG</u>	(exons MS4A6A)				397
A6E	V	H	S	S	L	A	G	S	I	L	S	A	L	S	A	L	V	G	F	I	
A6E	<u>GTG</u>	<u>CAT</u>	<u>AGC</u>	<u>AGC</u>	<u>CTG</u>	<u>GCT</u>	<u>GGA</u>	<u>AGC</u>	<u>ATT</u>	<u>CTG</u>	<u>AGT</u>	<u>GCT</u>	<u>CTG</u>	<u>TCT</u>	<u>GCC</u>	<u>CTG</u>	<u>GTG</u>	<u>GGT</u>	<u>TTC</u>	<u>ATT</u>	221
A6A	<u>GTG</u>	<u>CAT</u>	<u>AGC</u>	<u>AGC</u>	<u>CTG</u>	<u>GTT</u>	<u>GGA</u>	<u>AGC</u>	<u>ATT</u>	<u>CTG</u>	<u>AGT</u>	<u>GCT</u>	<u>CTG</u>	<u>TCT</u>	<u>GCC</u>	<u>CTG</u>	<u>GTG</u>	<u>GGT</u>	<u>TTC</u>	<u>ATT</u>	637
A6E	L	L	S	V	N	P	A	A	L	N	P	A	S	L	Q	C	K	L	D	E	
A6E	<u>CTC</u>	<u>CTG</u>	<u>TCT</u>	<u>GTC</u>	<u>AAC</u>	<u>CCG</u>	<u>GCT</u>	<u>GCA</u>	<u>TTA</u>	<u>AAT</u>	<u>CCT</u>	<u>GCC</u>	<u>TCA</u>	<u>TTG</u>	<u>CAG</u>	<u>TGT</u>	<u>AAG</u>	<u>TTG</u>	<u>GAC</u>	<u>GAA</u>	281
A6A	<u>ATC</u>	<u>CTG</u>	<u>TCT</u>	<u>GTC</u>	<u>AAA</u>	<u>CAG</u>	<u>GCC</u>	<u>ACC</u>	<u>TTA</u>	<u>AAT</u>	<u>CCT</u>	<u>GCC</u>	<u>TCA</u>	<u>CTG</u>	<u>CAG</u>	<u>TGT</u>	<u>GAG</u>	<u>TTG</u>	<u>GAC</u>	<u>AAA</u>	697
A6E	K	D	I	P	T	R	L	L	L	S	Y	D	Y	H		S	P	Y	T	M	
A6E	AAG	GAT	ATA	CCA	ACC	AGA	CTT	CTT	CTT	TCT	TAT	GAT	TAT	CAT		TCA	CCT	TAC	ACC	ATG	338
A6A	AAT	AAT	ATA	CCA	ACA	AGA	AGT	TAT	GTT	TCT	TAC	TTT	TAT	CAT	GAT	TCA	CTT	TAT	ACC	ACG	757
A6E	D	C	H	R	A	K	A	S	L	A	G	T	L	S	L	M	L	V	S	T	
A6E	GAC	TGC	CAT	AGA	GCC	AAA	GCC	AGT	<u>CTG</u>	<u>GCT</u>	<u>GGA</u>	<u>ACT</u>	<u>CTG</u>	<u>TCT</u>	<u>CTG</u>	<u>ATG</u>	<u>CTG</u>	<u>GTT</u>	<u>TCT</u>	<u>ACT</u>	398
A6A	GAC	TGC	TAT	ACA	GCC	AAA	GCC	AGT	<u>CTG</u>	<u>GCT</u>	<u>GGA</u>	<u>ACT</u>	<u>CTC</u>	<u>TCT</u>	<u>CTG</u>	<u>ATG</u>	<u>CTG</u>	<u>ATT</u>	<u>TGC</u>	<u>ACT</u>	817
A6E	V	L	E	F	C	L	A	V	L	T	A	V	L	Q	W	K	Q	T	V	*	
A6E	<u>GTG</u>	<u>TTG</u>	<u>GAG</u>	<u>TTC</u>	<u>TGC</u>	<u>CTA</u>	<u>GCT</u>	<u>GTG</u>	<u>CTC</u>	<u>ACT</u>	<u>GCT</u>	<u>GTG</u>	<u>CTG</u>	<u>CAG</u>	<u>TGG</u>	<u>AAA</u>	<u>CAG</u>	<u>ACT</u>	<u>GTC</u>	<u>TGA</u>	458
A6A	<u>CTG</u>	<u>CTG</u>	<u>GAA</u>	<u>TTC</u>	<u>TGC</u>	<u>CTA</u>	<u>GCT</u>	<u>GTG</u>	<u>CTC</u>	<u>ACT</u>	<u>GCT</u>	<u>GTG</u>	<u>CTG</u>	<u>CGG</u>	<u>TGG</u>	<u>AAA</u>	<u>CAG</u>	<u>GCT</u>	<u>TAC</u>	<u>TCT</u>	877
A6E	C	TTC	CCT	GG													TTA	CTC	ATG	TCC	479
A6A	GAC	TTC	CCT	GGG	AGT	GTA	CTT	TTC	CTG	CCT	CAC	AGT	TAC	ATT	GGT	AAT	TCT	GGC	ATG	TCC	937
A6E	TCA	AAG	ACG	ACT	CAT	GAT	GCT	GGA	TAT	GAA	GAA	CTA	TTG	ACT	TCT	TGG	GAA	AAA	ACG	GAG	539
A6A	TCA	AAA	ATG	ACT	CAT	GAC	TGT	GGA	TAT	GAA	GAA	CTA	TTG	ACT	TCT	TAA	GAA	AAA	AGG	GAG	997
A6E	AAA	TAT	TAA	TTG	GAA	AGT	TGA	TTT	TTA	TGA	TAA	TAT	GGA	AAA	CCT	AAC	CAT	TAT	AAA	AAA	599
A6A	AAA	TAT	TAA	TCA	GAA	AGT	TGA	TTC	TTA	TGA	TAA	TAT	GGA	AAA	GTT	AAC	CAT	TAT	AGA	AAA	1057
A6E	GCA	AA	CTT	GAG	TTT	CCT	AAA	TGT	AAG	CAT	TTA	AAG	TAA	ATG	CAT	ATT	TGT	TTT	AAA	AAA	658
A6A	GCA	AAG	CTT	GAG	TTT	CCT	AAA	TGT	AAG	CTT	TTA	AAG	TAA	TG	AAC	ATT	AA	AAA	AAA	CCA	1115
A6E	TTA																				661
A6A	TTA	TTT	CAC	TGT	CA																1129

A10	C CAG GGC CCC CAT CCA GCA TCA																				22
a10	C CAG GGT TCC CGG CCA GGG TCA																				74
A10	M	K	A	E		A	T	V	I	P	S	R	C	A	R	G	L	P	S	W	
A10	ATG	AAA	GCA	GAA		GCC	ACA	GTT	ATT	CCC	AGC	CGT	TGT	GCT	AGG	GGG	CTC	CCA	TCA	TGG	79
a10	ATG	GCT	GGC	CAA	GCT	CCC	ACA	GCG	GTT	CCC	GGC	AGT	GTT	ACT	GGA	GAA	GTC	TCA	CGA	TGG	134
A10	Q	V	L	S	P	V	Q	P	W	Q	T	S	A	P	Q	N	T	T	Q	P	
A10	CAA	GTC	CTC	AGC	CCA	GTC	CAG	CCC	TGG	CAG	ACA	AGT	GCA	CCC	CAG	AAC	ACG	ACC	CAG	CCC	139
a10	CAG	AAC	CTA	GGA	CCT	GCC	CAG	CCT	GCA	CAG	AAA	GTA					GCC	CAG	CCC	179	
A10	K	L	L	A	P	H	Q	H		E	K	S	Q	K	K	S	S	L	L	K	
A10	AAG	CTC	CTG	GCT	CCA	CAC	CAG	CAC		GAG	AAG	TCC	CAG	AAG	AAG	AGC	AGC	CTT	CTT	AAG	196
a10	CAA	AAC	CTG	GTT	CCA	GAT	GGG	CAC	CTT	GAG	AAA	GCC	CTG	GAG	GGA	AGT	GAC	CTT	CTA	CAG	239
A10	E	L	G	A	F	H	I	T	I	A	L	L	H	L	V	F	G	G	Y	L	
A10	GAG	CTG	GGG	GCC	TTC	CAC	ATC	ACC	ATC	GCT	CTG	CTG	CAC	CTG	GTC	TTT	GGG	GGC	TAC	CTG	256
a10	AAG	TTG	GGT	GGC	TTT	CAC	ATC	GCC	ATT	GCT	TTT	GCA	CAC	TTG	GCC	TTT	GGT	GGC	TAC	TTG	299
A10	A	S	I	V	K	N	L	H	L	V	V	L	K	S	W	Y	P	F	W	G	
A10	GCC	TCT	ATA	GTC	AAG	AAC	CTT	CAC	CTG	GTG	GTG	CTG	AAG	TCT	TGG	TAT	CCA	TTC	TGG	GGG	316
a10	ATC	TCC	ACA	GTC	AAG	AAT	CTG	CAC	CTG	GTG	GTG	TTG	AAG	TGC	TGG	TAT	CCA	CTC	TGG	GGA	359
A10	A	A	S	F	L	I	S	G	I	L	A	I	T	M	K	T	F	S	K	T	
A10	GCT	GCC	TCT	TTT	CTC	ATT	TCA	GGG	ATC	TTG	GCG	ATA	ACA	ATG	AAG	ACC	TTT	TCT	AAA	ACT	376
a10	ACT	GTC	TCT	TTT	CTC	GTT	GCA	GGG	ATG	GCG	GCC	ATG	ACA	ACA	GTG	ACA	TTC	CCT	AAG	ACC	419
A10	Y	L	K	M	L	C	L	M	T	N	L	I	S	L	F	C	V	L	S	G	
A10	TAC	CTG	AAG	ATG	TTG	TGC	CTG	ATG	ACA	AAC	CTC	ATC	AGC	CTC	TTT	TGC	GTG	CTG	TCT	GGC	436
a10	TCT	CTG	AAG	GTT	CTC	TGT	GTG	ATA	GCC	AAC	GTT	ATC	AGC	TTG	TTC	TGC	GCA	CTG	GCC	GGC	479
A10	L	F	V	I	S	K	D	L	F	L	E	S	P	F	E	S	P	I	W	R	
A10	CTC	TTC	GTC	ATC	TCC	AAG	GAT	CTC	TTT	CTG	GAG	AGC	CCA	TTT	GAG	TCC	CCG	ATC	TGG	AGA	496
a10	TTC	TTT	GTC	ATT	GCC	AAG	GAC	CTC	TTC	CTG	GAG	GGT	CCT	TTT	CCA	TGG	CCA	ATC	TGG	AGA	539
A10	M	Y	P	N	S	T	V	H	I	Q	R	L	E	L	A	L	L	C	F	T	
A10	ATG	TAC	CCC	AAC	TCC	ACG	GTC	CAC	ATC	CAG	AGG	CTG	GAG	CTG	GCC	TTG	CTC	TGC	TTC	ACT	556
a10	CCA	TAC	CCT	GAA	CCC	ACA	ACC	TAC	ATC	CAA	AGG	CTA	GAG	CTG	ACC	CTG	TTC	TGC	TTC	ACC	599
A10	V	L	E	L	F	L	P	V	P	T	A	V	T	A	W	R	G	D	C	P	
A10	GTC	CTA	GAG	CTC	TTC	CTG	CCA	GTG	CCC	ACA	GCT	GTC	ACA	GCC	TGG	AGA	GGG	GAC	TGC	CCA	616
a10	TTT	CTG	GAG	ATC	TTC	CTG	TCG	GGG	TCC	ACA	GCC	ATC	ACA	GCC	TAT	AGG	ATG	AAA	CGC	CTG	659
A10	S	A	K		N	D	D	A	C	L	V	P	N	T	P	L	H	L	K	G	
A10	TCT	GCA	AAG		AAT	GAT	GAT	GCA	TGC	CTT	GTT	CCG	AAT	ACA	CCA	TTG	CAT	CTC	AAA	GGC	673
a10	CAA	GCA	GAG	GAC	AAG	GAT	GAC	ACC	CCT	TTC	GTT	CCT	GAC	ACA	CCT	ATG	GAA	CTT	AAA	GGT	719
A10	L	P	V	E	P	P	P	S	Y	Q	S	V	I	Q	G	D	A	Q	H	K	
A10	CTG	CCG	GTG	GAG	CCC	CCG	CCA	TCC	TAC	CAG	AGT	GTG	ATT	CAA	GGC	GAC	GCA	CAA	CAC	AAG	733
a10	CTA	TCG	CTG	GGG	CCA	CCA	CCA	TCC	TAT	AAA	GAT	GTG	GCC	CAA	GGA	CAC	TCC	TCC	TCT	GAT	779
A10	Q	H	Q	R	*																
A10	CAA	CAT	CAG	AGG	TGA	AGA	GGT	TTG	GCC	CTG	GCT	CCC	CAG	ACC	TTC	AGA	ACC	CAC	GCT	TGG	793
a10	ACT	GGC	AGA	GCC	TTG	GCC	ACC	AGC	TCT	GGA	CTG	CTG	CTG	GCC	TCT	GAC	TCC	TTC	CAT	CAA	839
A10	CCC	CTT	CTC	CCT	GGC	ATA	GAT	AGA	AAC	CAG	TTC	CCA	GGG	GAGCTGTAAG	GGGCAAGGGG						852
a10	GCT	CTG	CTT	CAC	ACG	GGC	CCA	AGG	ACC	TTG	AGA	AAG	TAG	TCTAAGACTA	CTAGACTTTC						898
A10	CTAACAGTGC	TGCAGCTAGA	ACTGCCTGGC	CTGGGAGTGG	TAGCCAAGGC	AGCAATGGTC	CTATCCCCTC														922
a10	CCAAATAAAGA	CTGAGTTCCT	GCAATGCCAA	GTCCTTCCCT	GCCTCCCATT	GGCTGGACTC	CGGTGATGAC														968
A10	AGGCACTAGA	GGAACCTCCA	GGGCCCCCA	GGAACATCTC	AGCACCTGAC																972
a10	ACAGGCGTGA	CTTGCACA	AA TAAATGCATA	ACCACTATGA	AAAAAAAAA																1018

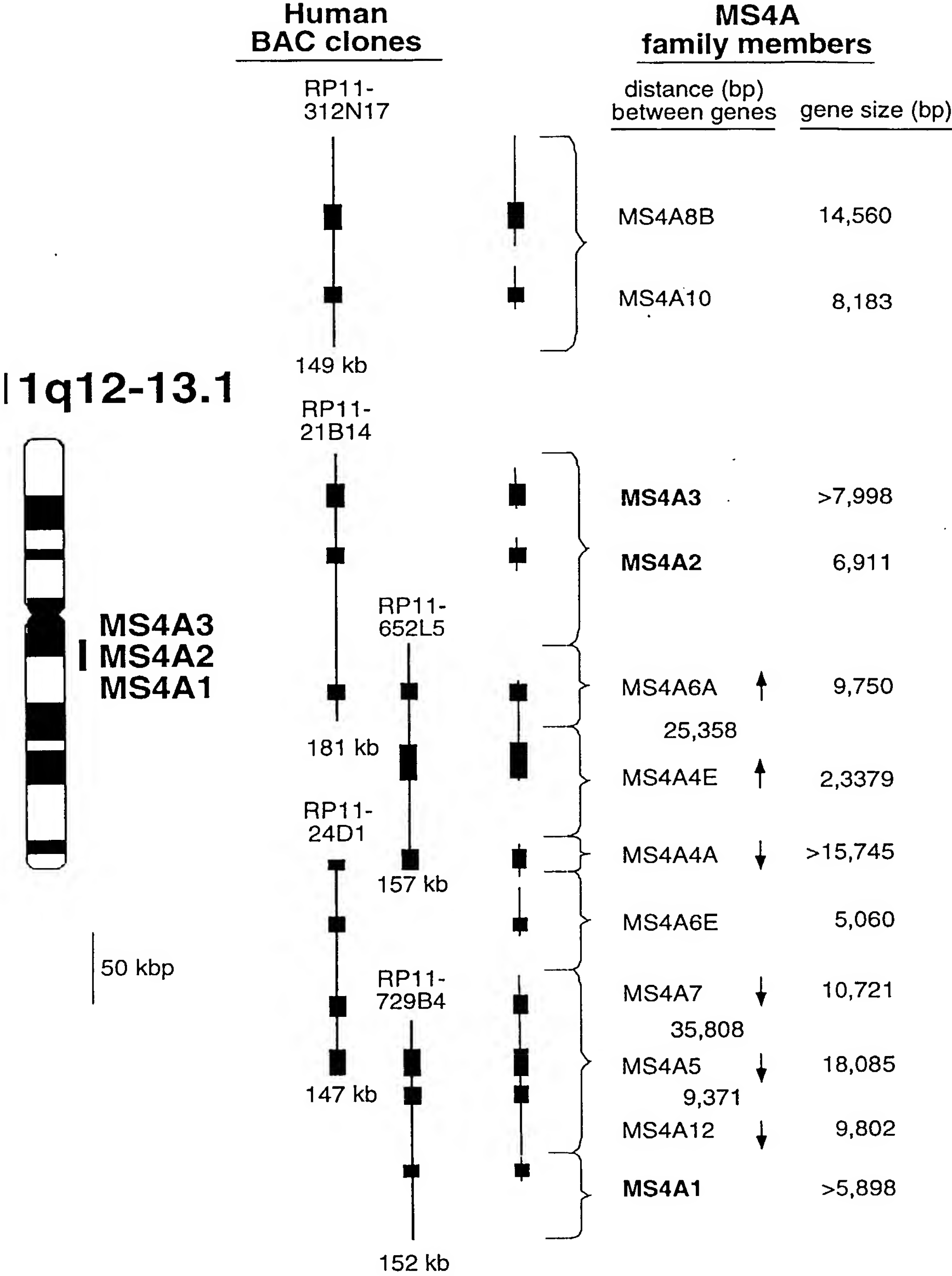


Figure 6



Figure 7

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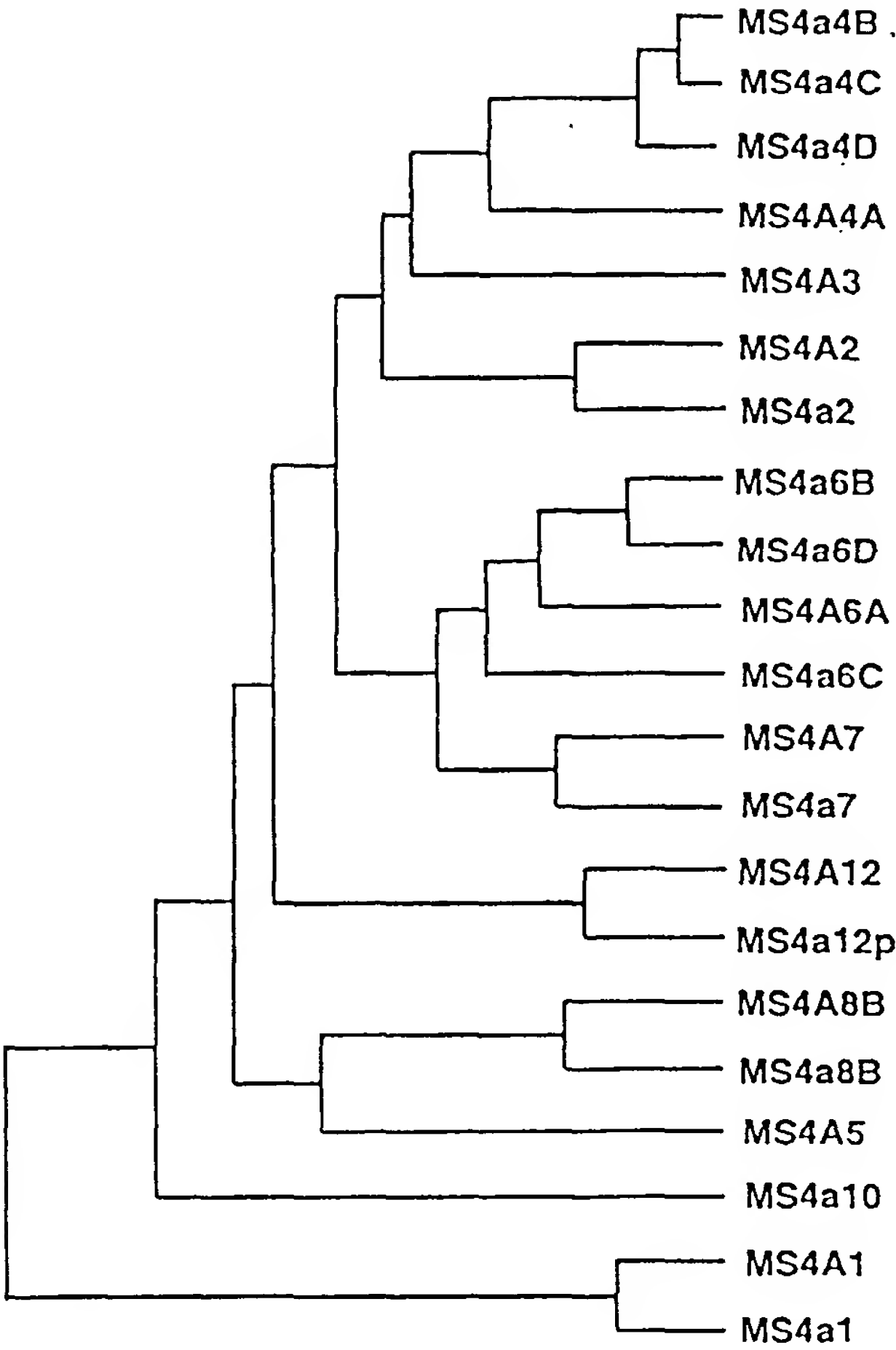
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A2 MDTESNRRANLALP QEPS SVPAFEVLEISQEVSSGRLLKSASSPPLHTWLTVLKKEQEFGL VTQILTAMICLCFGTIVCSVLDI 85
a2 MDTENRSRADLALPNQESS SAPDIELLEASP AKAAPPKQTWRTFLKKELEFLG ATQILVGLICLCFGTIVCSVLVY 77
A3 MASHEVDNAELGSASAHGTPGSETGPEELNTSVYHPINGSPDYQKAKLVGLG AIQILNAAMILALGVFLGSLQYP 75
a3 MKPEETGGSVYQPLDESRHVQRGVQLALG AIQILNGLILALGIFLVLCQHV 52
A4A MTTMQGMEQAMPAGPGVPQPLGNMAVIHSHLWKGLQEKFLKGEKVLG VVQILTALMSLSMGITMCMASN 71
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A5 MDSSTAHSVPVFLVFPPEITASEYESTELSTATTSTQSLQKLFARKMKILG TIQILFGIMTFSFGVIFLFTLLK 74
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a7 MRLQLGTKNIGWDCFPKDI I HKREKTGHTYEKEDDLLIGVPSEATLLG TIQILCALILASFGGILVSASY 71
A8B MNSMSTSAVPVANSVLVAPHNGYPVTPGIMSHVPLVNSQPVHVLVPGNPPSLVSNVNGQPVQKALKEGKTLG AIQIIIGLAHIGLSIMATVLVG 96
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Figure 8





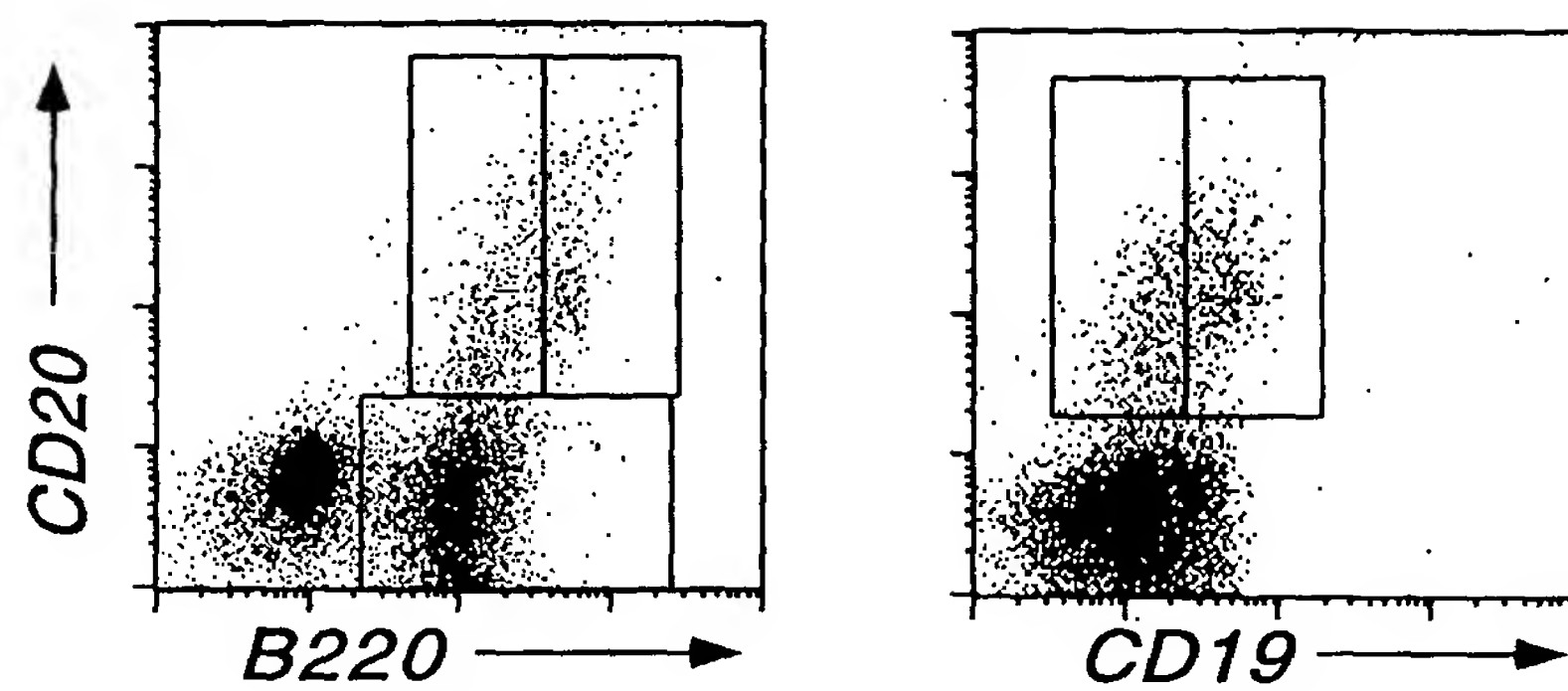
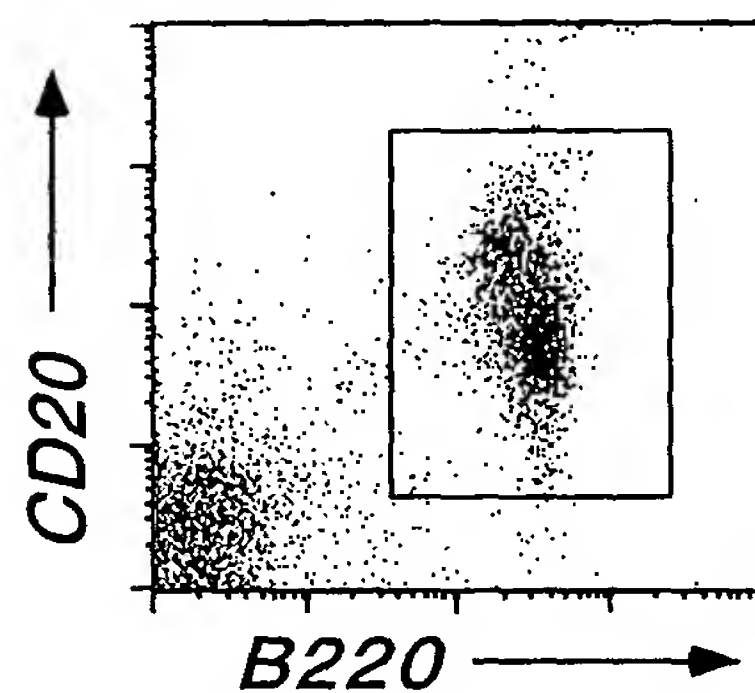
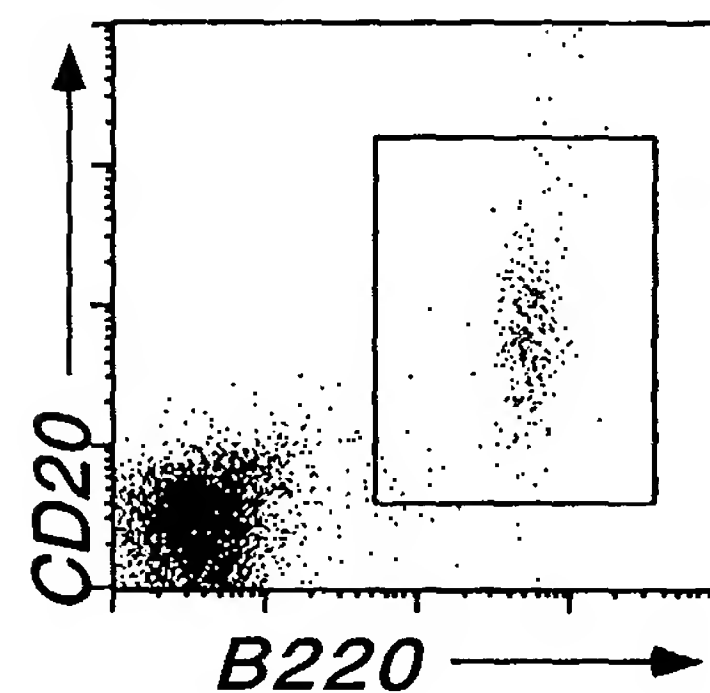
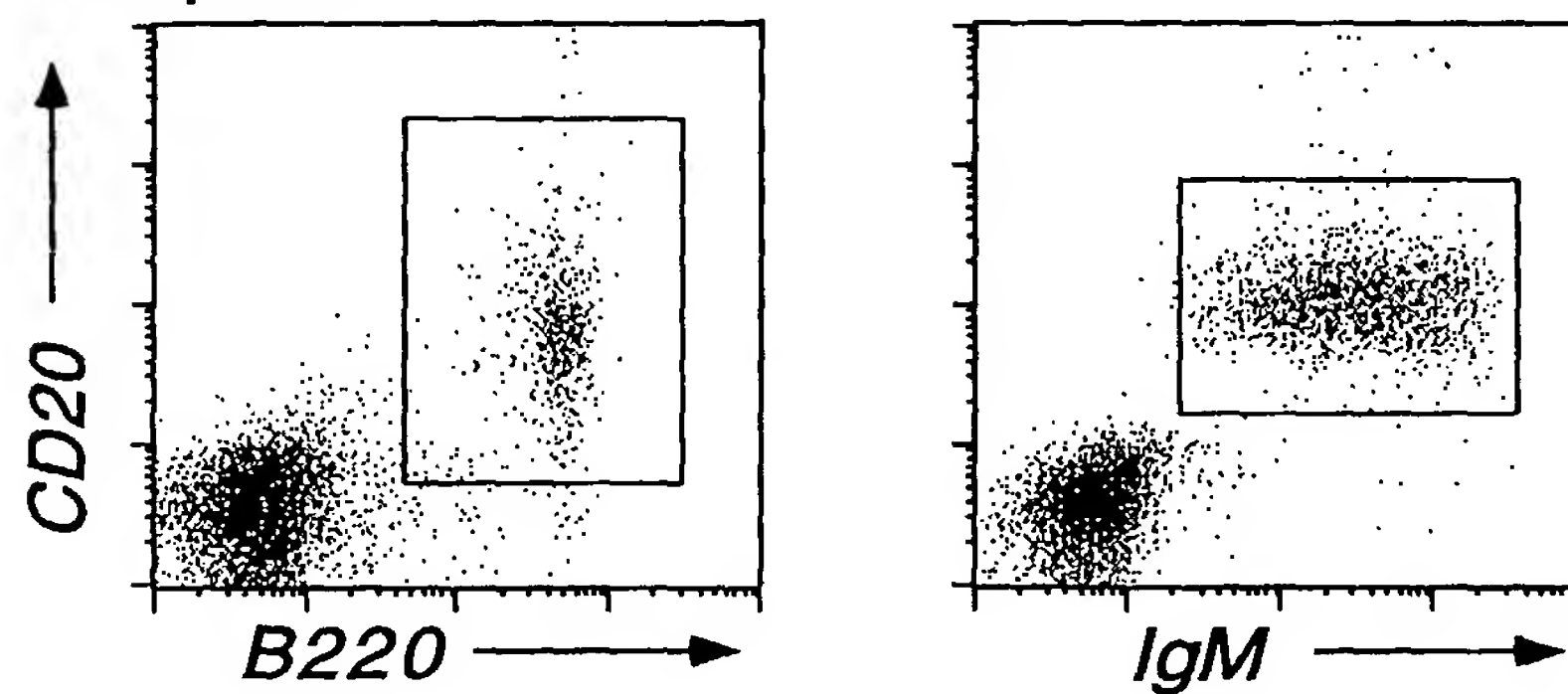
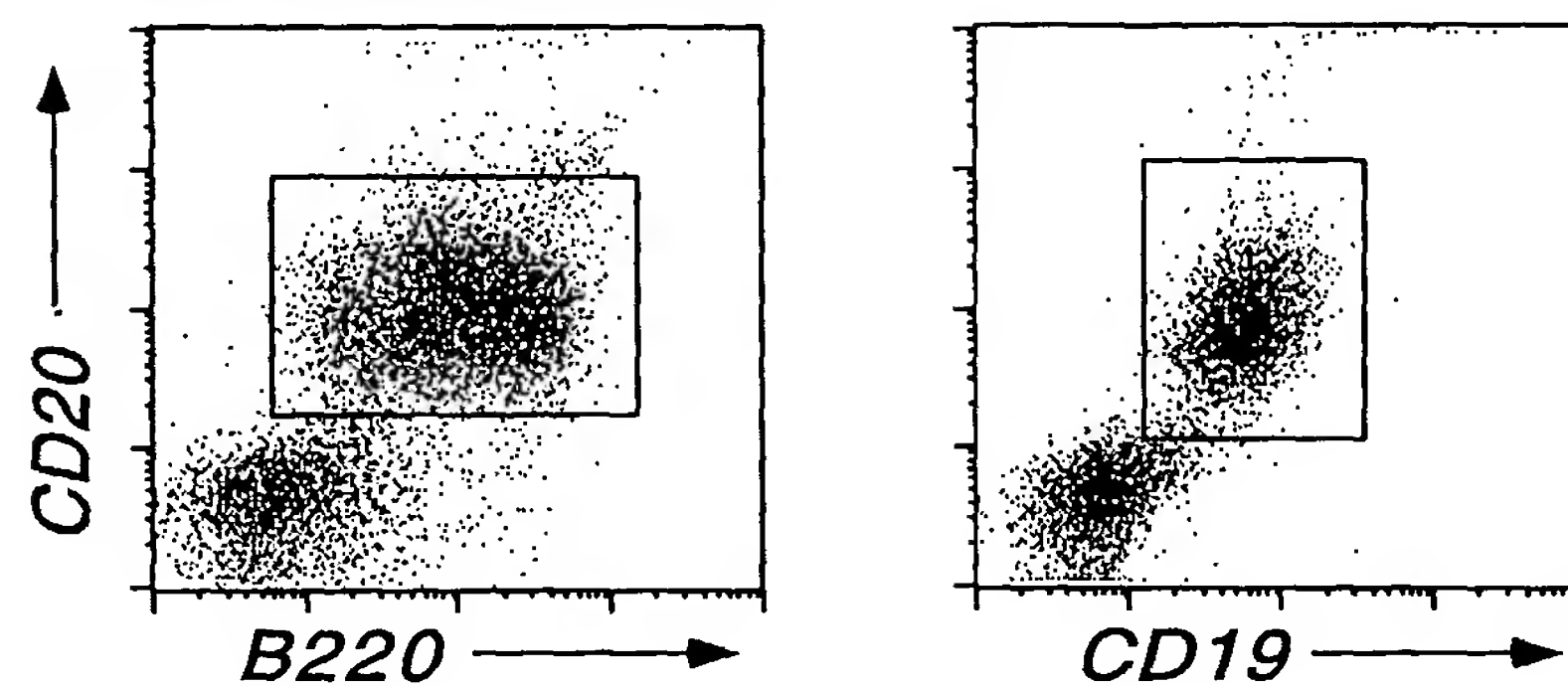
**A. Bone Marrow****B. Blood****C. PLN****D. Spleen****E. Peritoneal Lavage**

Figure 9

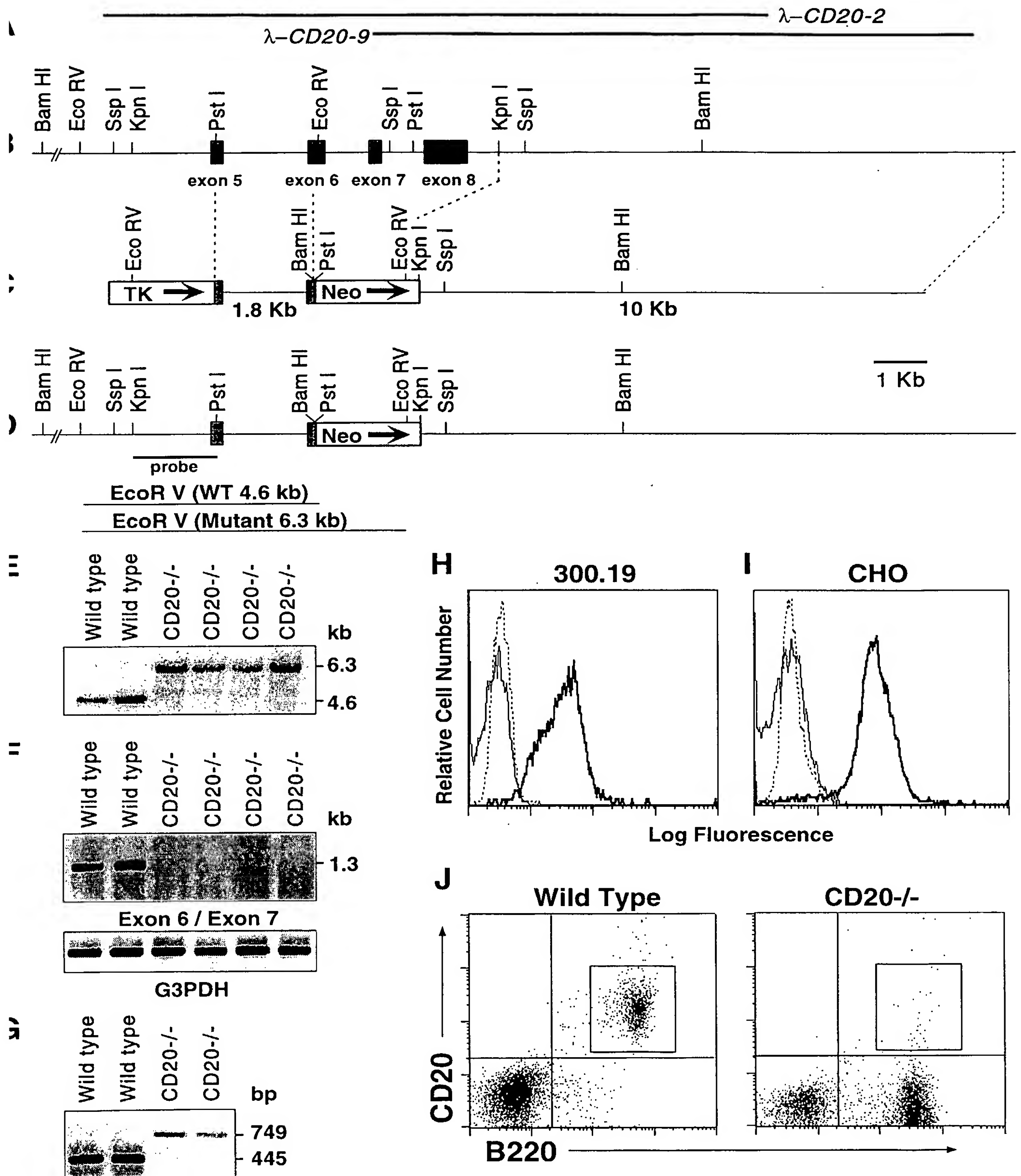


Figure 10

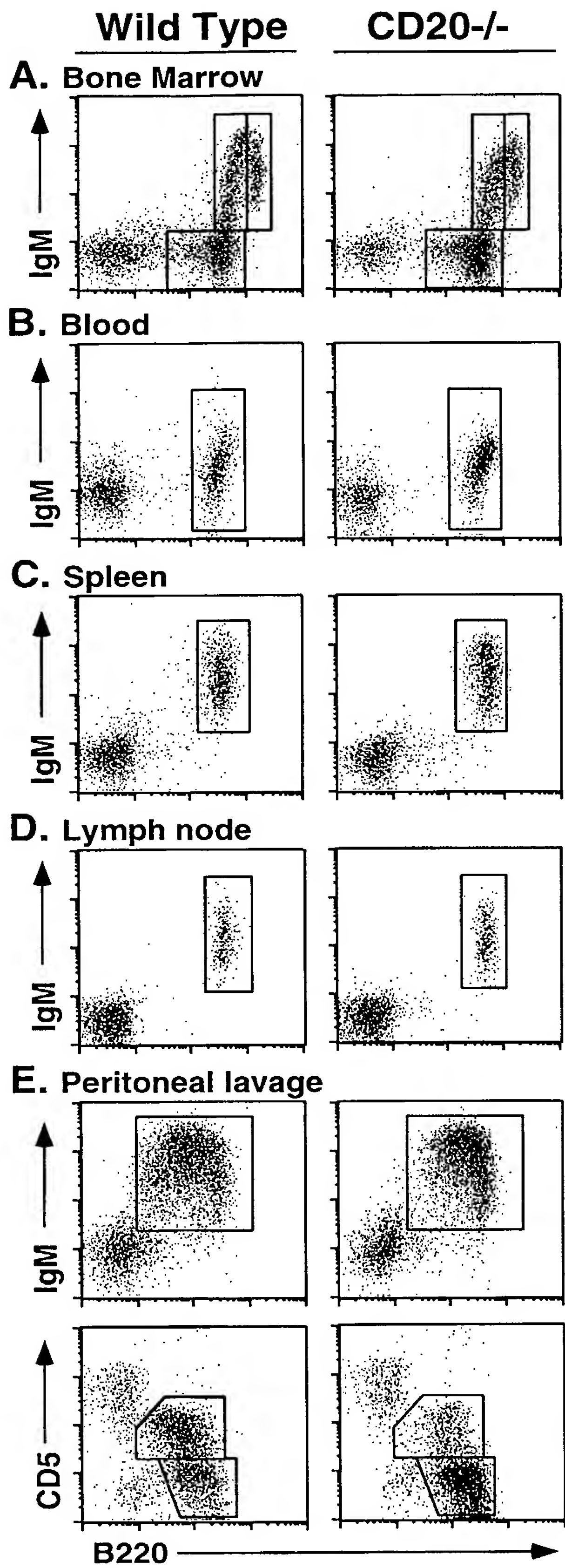


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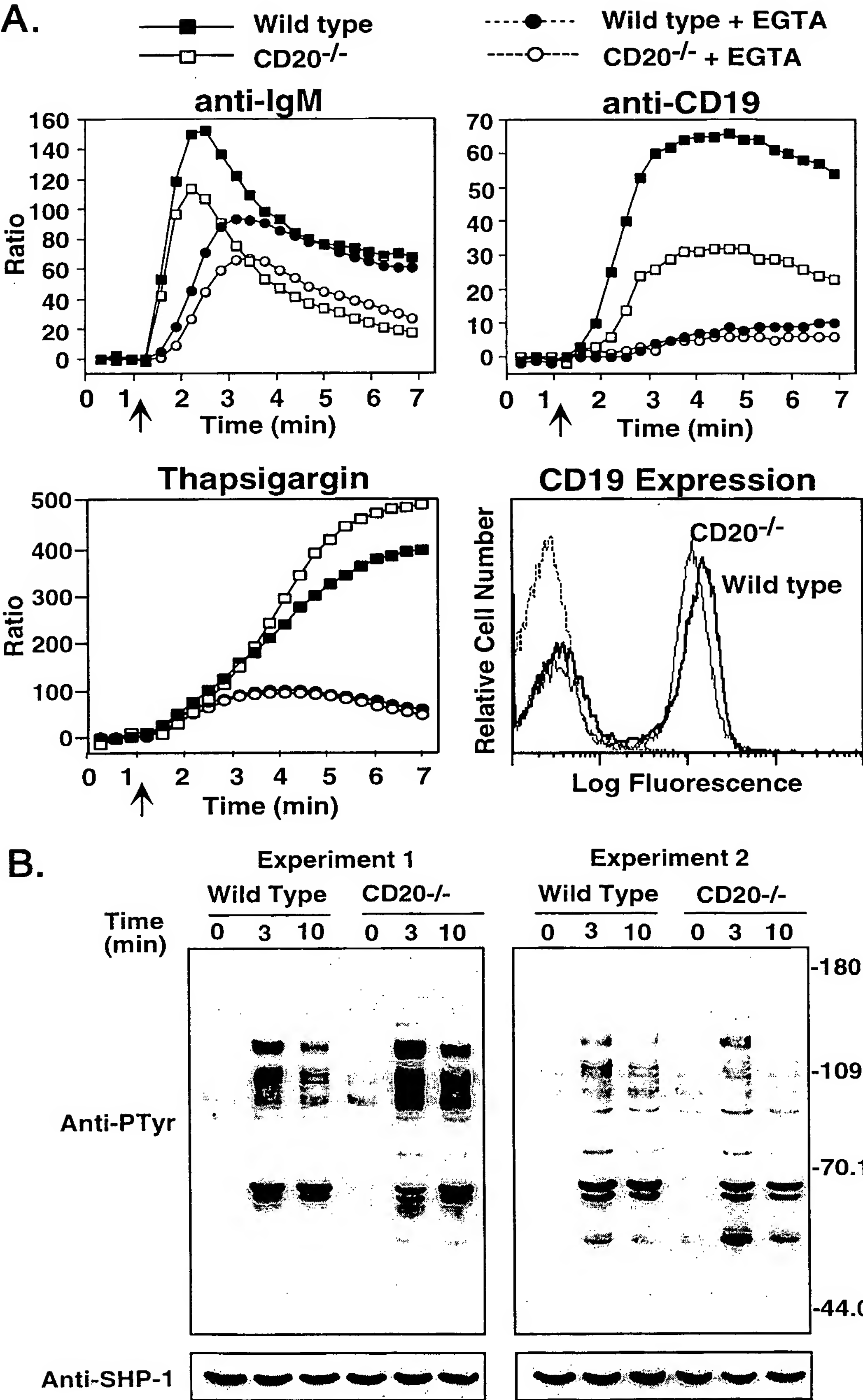


Figure 12

Sequence Listing

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Liang, Yinghua

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	ctttcagaag	atgaaggtaa	gtagaaaccg	ttgatgggac	tgagaaacca	gagttaaaac	180										
55	ctctttggag	cttctgagga	ctcagctgga	accaacgggc	acagttggca	acaccatc	238										
	atg aca tca caa cct gtt ccc aat gag acc atc ata gtg ctc cca tca	286															
	Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser																
60	1	5	10	15													
	aat gtc atc aac ttc tcc caa gca gag aaa ccc gaa ccc acc aac cag	334															

	Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln		
				20					25					30				
5	ggg Gly	cag Gln	gat Asp 35	agc Ser	ctg Leu	aag Lys	aaa Lys	cat His 40	cta Leu	cac His	gca Ala	gaa Glu	att Ile 45	aaa Lys	gtt Val	att Ile	382	
10	ggg Gly	act Thr 50	atc Ile	cag Gln	atc Ile	ttg Leu	tgt Cys 55	ggc Gly	atg Met	atg Met	gta Val	ttg Leu 60	agc Ser	ttg Leu	ggg Gly	atc Ile	430	
15	att Ile 65	ttg Leu	gca Ala	tct Ser	gct Ala	tcc Ser 70	ttc Phe	tct Ser	cca Pro	aat Asn	ttt Phe 75	acc Thr	caa Gln	gtg Val	act Thr	tct Ser 80	478	
20	aca Thr	ctg Leu	ttg Leu	aac Asn	tct Ser 85	gct Ala	tac Tyr	cca Pro	ttc Phe	ata Ile 90	gga Gly	ccc Pro	ttt Phe	ttt Phe	ttt Phe 95	atc Ile	526	
25	atc Ile	tct Ser	ggc Gly	tct Ser 100	cta Leu	tca Ser	atc Ile	gcc Ala 105	aca Thr	gag Glu	aaa Lys	agg Arg	tta Leu	acc Thr 110	aag Lys	ctt Leu	574	
30	ttg Leu	gtg Val	cat His 115	agc Ser	agc Ser	ctg Leu	gtt Val 120	gga Gly 125	agc Ser	att Ile	ctg Leu	agt Ser 125	gct Ala 125	ctg Leu	tct Ser	gcc Ala	622	
35	ctg Leu	gtg Val 130	ggc Gly	ttc Phe	att Ile	atc Ile	ctg Leu 135	tct Ser	gtc Val	aaa Lys	cag Gln	gcc Ala 140	acc Thr	tta Leu	aat Asn	cct Pro	670	
40	gcc Ala 145	tca Ser	ctg Leu	cag Gln	tgt Cys	gag Glu 150	ttg Leu	gac Asp	aaa Lys	aat Asn	aat Asn 155	ata Ile	cca Pro	aca Thr	aga Arg	agt Ser 160	718	
45	tat Tyr	gtt Val	tct Ser	tac Tyr	ttt Phe 165	tat Tyr	cat His	gat Asp	tca Ser	ctt Leu 170	tat Tyr	acc Thr	acg Thr	gac Asp	tgc Cys 175	tat Tyr	766	
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55	act Thr	ctg Leu	ctg Leu 195	gaa Glu	ttc Phe	tgc Cys	cta Leu 200	gct Ala 200	gtg Val	ctc Leu	act Thr	gct Ala 205	gtg Val 205	ctg Leu	cgg Arg	tgg Trp	862	
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65	agt Ser 225	tac Tyr	att Ile	ggc Gly	aat Asn	tct Ser 230	ggc Gly	atg Met	tcc Ser	tca Ser	aaa Lys 235	atg Met	act Thr	cat His	gac Asp	tgt Cys 240	958	
70	gga Gly	tat Tyr	gaa Glu	gaa Glu	cta Leu	ttg Leu	act Thr	tct Ser	tta Ser	gaaaaaaggg agaaatatta							1005	
75	atcagaaaagt tgattcttat gataatatgg aaaagttaac cattatagaa aagcaaagct																	1065

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&lt;210&gt; 8

&lt;211&gt; 248

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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&lt;400&gt; 8

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Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser  
 1 5 10 15

Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln  
 20 25 30

25

Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile  
 35 40 45

30

Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile  
 50 55 60

35

Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser  
 65 70 75 80

40

Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile  
 85 90 95

Ile Ser Gly Ser Leu Ser Ile Ala Thr Glu Lys Arg Leu Thr Lys Leu  
 100 105 110

45

Leu Val His Ser Ser Leu Val Gly Ser Ile Leu Ser Ala Leu Ser Ala  
 115 120 125

50

Leu Val Gly Phe Ile Ile Leu Ser Val Lys Gln Ala Thr Leu Asn Pro  
 130 135 140

55

Ala Ser Leu Gln Cys Glu Leu Asp Lys Asn Asn Ile Pro Thr Arg Ser  
 145 150 155 160

60

Tyr Val Ser Tyr Phe Tyr His Asp Ser Leu Tyr Thr Thr Asp Cys Tyr  
 165 170 175

-12-

	45		50		55		60	
5	agc ttg ggg atc att ttg gca tct gct tcc ttc tct cca aat ttt acc Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr	244						
		65		70		75		
10	caa gtg act tct aca ctg ttg aac tct gct tac cca ttc ata gga ccc Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro	292						
		80		85		90		
15	ttt ttt ttt atc atc tct ggc tct cta tca atc gcc aca gag aaa agg Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala Thr Glu Lys Arg	340						
		95		100		105		
20	tta acc aag ctt ttg gtg cat agc agc ctg gtt gga agc att ctg agt Leu Thr Lys Leu Leu Val His Ser Ser Leu Val Gly Ser Ile Leu Ser	388						
		110		115		120		
25	gct ctg tct gcc ctg gtg ggt ttc att atc ctg tct gtc aaa cag gcc Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu Ser Val Lys Gln Ala	436						
		125		130		135		140
30	acc tta aat cct gcc tca ctg cag tgt gag ttg gac aaa aat aat ata Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu Asp Lys Asn Asn Ile	484						
		145		150		155		
35	cca aca aga agt tat gtt tct tac ttt tat cat gat tca ctt tat acc Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His Asp Ser Leu Tyr Thr	532						
		160		165		170		
40	acg gac tgc tat aca gcc aaa gcc agt ctg gct gga tct ctc tct ctg Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala Gly Ser Leu Ser Leu	580						
		175		180		185		
45	atg ctg att tgc act ctg ctg gaa ttc tgc cta gct gtg ctc act gct Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Leu Ala Val Leu Thr Ala	628						
		190		195		200		
50	gtg ctg cgg tgg aaa cag gct tac tct gac ttc cct ggg agt gta ctt Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe Pro Gly Ser Val Leu	676						
		205		210		215		220
55	ttc ctg cct cac agt tac att ggt aat tct ggc atg tcc tca aaa atg Phe Leu Pro His Ser Tyr Ile Gly Asn Ser Gly Met Ser Ser Lys Met	724						
		225		230		235		
60	act cat gac tgt gga tat gaa gaa cta ttg act tct taa gaaaaaaggg Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr Ser	773						
		240		245				
	agaaatatta atcagaaagt tgattcttat gataatatgg aaaagttaac cattatagaa	833						
	aagcaaagct tgagtttcct aaatgtaagc ttttaaagta atgaacatta aaaaaaacca	893						
	ttatttcact gtcaaaaaaa aaaaaaaaaa aaaaaaa	930						
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&lt;211&gt; 248

&lt;212&gt; PRT

5 &lt;213&gt; Homo sapiens

&lt;400&gt; 10

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Met	Thr	Ser	Gln	Pro	Val	Pro	Asn	Glu	Thr	Ile	Ile	Val	Leu	Pro	Ser
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Asn	Val	Ile	Asn	Phe	Ser	Gln	Ala	Glu	Lys	Pro	Glu	Pro	Thr	Asn	Gln
			20					25					30		

20

Gly	Gln	Asp	Ser	Leu	Lys	Lys	His	Leu	His	Ala	Glu	Ile	Lys	Val	Ile
		35					40					45			

25

Gly	Thr	Ile	Gln	Ile	Leu	Cys	Gly	Met	Met	Val	Leu	Ser	Leu	Gly	Ile
	50					55					60				

30

Ile	Leu	Ala	Ser	Ala	Ser	Phe	Ser	Pro	Asn	Phe	Thr	Gln	Val	Thr	Ser
65					70					75					80

Thr	Leu	Leu	Asn	Ser	Ala	Tyr	Pro	Phe	Ile	Gly	Pro	Phe	Phe	Phe	Ile
			85						90					95	

35

Ile	Ser	Gly	Ser	Leu	Ser	Ile	Ala	Thr	Glu	Lys	Arg	Leu	Thr	Lys	Leu
			100					105					110		

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Leu	Val	His	Ser	Ser	Leu	Val	Gly	Ser	Ile	Leu	Ser	Ala	Leu	Ser	Ala
		115					120					125			

45

Leu	Val	Gly	Phe	Ile	Ile	Leu	Ser	Val	Lys	Gln	Ala	Thr	Leu	Asn	Pro
	130					135					140				

Ala	Ser	Leu	Gln	Cys	Glu	Leu	Asp	Lys	Asn	Asn	Ile	Pro	Thr	Arg	Ser
145					150					155					160

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Tyr	Val	Ser	Tyr	Phe	Tyr	His	Asp	Ser	Leu	Tyr	Thr	Thr	Asp	Cys	Tyr
				165					170					175	

55

Thr	Ala	Lys	Ala	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Leu	Met	Leu	Ile	Cys
			180					185					190		

60

Thr	Leu	Leu	Glu	Phe	Cys	Leu	Ala	Val	Leu	Thr	Ala	Val	Leu	Arg	Trp
		195					200					205			



Lys Gln Ala Tyr Ser Asp Phe Pro Gly Ser Val Leu Phe Leu Pro His  
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Ser Tyr Ile Gly Asn Ser Gly Met Ser Ser Lys Met Thr His Asp Cys  
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Gly Tyr Glu Glu Leu Leu Thr Ser  
 245

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 Met Thr Ser Gln Pro Ile Ser Asn Glu Thr Ile Ile  
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atg ctc cca tca aat gtc atc aac ttc tcc caa gca gag aaa ccc gaa 98  
 Met Leu Pro Ser Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu  
 15 20 25

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ccc acc aac cag ggg cag gat agc ctg aag aaa cgt cta cag gca aaa 146  
 Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys Arg Leu Gln Ala Lys  
 30 35 40

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gtc aaa gtt att ggg gtg cat agc agc ctg gct gga agc att ctg agt 194  
 Val Lys Val Ile Gly Val His Ser Ser Leu Ala Gly Ser Ile Leu Ser  
 45 50 55 60

50

gct ctg tct gcc ctg gtg ggt ttc att ctc ctg tct gtc aac ccg gct 242  
 Ala Leu Ser Ala Leu Val Gly Phe Ile Leu Leu Ser Val Asn Pro Ala  
 65 70 75

55

gca tta aat cct gcc tca ttg cag tgt aag ttg gac gaa aag gat ata 290  
 Ala Leu Asn Pro Ala Ser Leu Gln Cys Lys Leu Asp Glu Lys Asp Ile  
 80 85 90

60

cca acc aga ctt ctt ctt tct tat gat tat cat tca cct tac acc atg 338  
 Pro Thr Arg Leu Leu Leu Ser Tyr Asp Tyr His Ser Pro Tyr Thr Met  
 95 100 105

5      gac tgc cat aga gcc aaa gcc agt ctg gct gga act ctg tct ctg atg      386  
        Asp Cys His Arg Ala Lys Ala Ser Leu Ala Gly Thr Leu Ser Leu Met  
           110                                   115                                   120

ctg gtt tct act gtg ttg gag ttc tgc cta gct gtg ctc act gct gtg      434  
 Leu Val Ser Thr Val Leu Glu Phe Cys Leu Ala Val Leu Thr Ala Val  
 125                                   130                                   135                                   140

10     ctg cag tgg aaa cag act gtc tga cttccctggg tactcatgtc ctcaaagacg      488  
        Leu Gln Trp Lys Gln Thr Val  
                                   145

15     actcatgatg ctggatatga agaactattg acttcttggg aaaaaacgga gaaatattaa      548  
        ttggaaagtt gatttttatg ataatatgga aaacctaacc attataaaaa agcaaacttg      608  
        agtttcctaa atgtaagcat tttaaagtaaa tgcataatttg ttttaaaaaa tta      661

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25     <212> PRT  
        <213> Homo sapiens

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Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln  
                                   20                                   25                                   30

40     Gly Gln Asp Ser Leu Lys Lys Arg Leu Gln Ala Lys Val Lys Val Ile  
                                   35                                   40                                   45

45     Gly Val His Ser Ser Leu Ala Gly Ser Ile Leu Ser Ala Leu Ser Ala  
                                   50                                   55                                   60

50     Leu Val Gly Phe Ile Leu Leu Ser Val Asn Pro Ala Ala Leu Asn Pro  
        65                                   70                                   75                                   80

55     Ala Ser Leu Gln Cys Lys Leu Asp Glu Lys Asp Ile Pro Thr Arg Leu  
                                   85                                   90                                   95

Leu Leu Ser Tyr Asp Tyr His Ser Pro Tyr Thr Met Asp Cys His Arg  
                                   100                                   105                                   110

60     Ala Lys Ala Ser Leu Ala Gly Thr Leu Ser Leu Met Leu Val Ser Thr

	115	120	125	
5	Val Leu Glu Phe Cys Leu Ala Val Leu Thr Ala Val Leu Gln Trp Lys	130	135	140
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45	atg cta tta caa tcc caa acc atg ggg gtt tct cac agc ttt aca cca			165
	Met Leu Leu Gln Ser Gln Thr Met Gly Val Ser His Ser Phe Thr Pro			
	1 5 10 15			
50	aag ggc atc act atc cct caa aga gag aaa cct gga cac atg tac caa			213
	Lys Gly Ile Thr Ile Pro Gln Arg Glu Lys Pro Gly His Met Tyr Gln			
	20 25 30			
	aac gaa gat tac ctg cag aac ggg ctg cca aca gaa acc acc gtt ctt			261
	Asn Glu Asp Tyr Leu Gln Asn Gly Leu Pro Thr Glu Thr Thr Val Leu			
	35 40 45			
55	ggg act gtc cag atc ctg tgt tgc ctg ttg att tca agt ctg ggg gcc			309
	Gly Thr Val Gln Ile Leu Cys Cys Leu Leu Ile Ser Ser Leu Gly Ala			
	50 55 60			
60	atc ttg gtt ttt gct ccc tac ccc tcc cac ttc aat cca gca att tcc			357
	Ile Leu Val Phe Ala Pro Tyr Pro Ser His Phe Asn Pro Ala Ile Ser			
	65 70 75 80			

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10	att act gga tcc ctc tca att atc tct gga aaa caa tca act aag ccc Ile Thr Gly Ser Leu Ser Ile Ile Ser Gly Lys Gln Ser Thr Lys Pro 100 105 110	453
15	ttt gac ctg agc agc ttg acc tca aat gca gtg agt tct gtt act gca Phe Asp Leu Ser Ser Leu Thr Ser Asn Ala Val Ser Ser Val Thr Ala 115 120 125	501
20	gga gca ggc ctc ttc ctc ctt gct gac agc atg gta gcc ctg agg act Gly Ala Gly Leu Phe Leu Leu Ala Asp Ser Met Val Ala Leu Arg Thr 130 135 140	549
25	gcc tct caa cat tgt ggc tca gaa atg gat tat cta tcc tca ttg cct Ala Ser Gln His Cys Gly Ser Glu Met Asp Tyr Leu Ser Ser Leu Pro 145 150 155 160	597
30	tat tcg gag tac tat tat cca ata tat gaa atc aaa gat tgt ctc ctg Tyr Ser Glu Tyr Tyr Tyr Pro Ile Tyr Glu Ile Lys Asp Cys Leu Leu 165 170 175	645
35	acc agt gtc agt tta aca ggt gtc cta gtg gtg atg ctc atc ttc act Thr Ser Val Ser Leu Thr Gly Val Leu Val Val Met Leu Ile Phe Thr 180 185 190	693
40	gtg ctg gag ctc tta tta gct gca tac agt tct gtc ttt tgg tgg aaa Val Leu Glu Leu Leu Leu Ala Ala Tyr Ser Ser Val Phe Trp Trp Lys 195 200 205	741
45	cag ctc tac tcc aac aac cct ggg agt tca ttt tcc tcg acc cag tca Gln Leu Tyr Ser Asn Asn Pro Gly Ser Ser Phe Ser Ser Thr Gln Ser 210 215 220	789
50	caa gat cat atc caa cag gtc aaa aag agt tct tca cgg tct tgg ata Gln Asp His Ile Gln Gln Val Lys Lys Ser Ser Ser Arg Ser Trp Ile 225 230 235 240	837
55	tta gtaactcttg gcctcagagg aaggaaaagc aactcaacac tcatgggtcaa gtgtgattag acttttcctga aatctctgcc atttttagata ctgtgaaaca aactaaaaaa aaaaaagctt ttgttttgta tttgtttact atgagtcggt atttaatttc tcttgaaaat aatttcctca aagcccaagt caataaatgt tatcagccag tcttccaaaa tggtcataaa ctttataaac tgctttgggt aaactgagca gaaggtgata cacagaaggg aaaatgtgca ctcatgctag tgtgaatttg gtaagtcgcg tgactctgca ggctgtttct gtattatttt cacactcata ttgcttaaatt attacatatt agggattg	890 950 1010 1070 1130 1190 1228
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&lt;211&gt; 240

&lt;212&gt; PRT

5 &lt;213&gt; Homo sapiens

&lt;400&gt; 14

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Met	Leu	Leu	Gln	Ser	Gln	Thr	Met	Gly	Val	Ser	His	Ser	Phe	Thr	Pro
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15

Lys	Gly	Ile	Thr	Ile	Pro	Gln	Arg	Glu	Lys	Pro	Gly	His	Met	Tyr	Gln
			20					25					30		

20

Asn	Glu	Asp	Tyr	Leu	Gln	Asn	Gly	Leu	Pro	Thr	Glu	Thr	Thr	Val	Leu
		35					40					45			

25

Gly	Thr	Val	Gln	Ile	Leu	Cys	Cys	Leu	Leu	Ile	Ser	Ser	Leu	Gly	Ala
	50					55					60				

30

Ile	Leu	Val	Phe	Ala	Pro	Tyr	Pro	Ser	His	Phe	Asn	Pro	Ala	Ile	Ser
65					70					75					80

Thr	Thr	Leu	Met	Ser	Gly	Tyr	Pro	Phe	Leu	Gly	Ala	Leu	Cys	Phe	Gly
				85					90					95	

35

Ile	Thr	Gly	Ser	Leu	Ser	Ile	Ile	Ser	Gly	Lys	Gln	Ser	Thr	Lys	Pro
			100					105					110		

40

Phe	Asp	Leu	Ser	Ser	Leu	Thr	Ser	Asn	Ala	Val	Ser	Ser	Val	Thr	Ala
		115					120					125			

45

Gly	Ala	Gly	Leu	Phe	Leu	Leu	Ala	Asp	Ser	Met	Val	Ala	Leu	Arg	Thr
	130					135					140				

Ala	Ser	Gln	His	Cys	Gly	Ser	Glu	Met	Asp	Tyr	Leu	Ser	Ser	Leu	Pro
145					150					155					160

50

Tyr	Ser	Glu	Tyr	Tyr	Tyr	Pro	Ile	Tyr	Glu	Ile	Lys	Asp	Cys	Leu	Leu
				165					170					175	

55

Thr	Ser	Val	Ser	Leu	Thr	Gly	Val	Leu	Val	Val	Met	Leu	Ile	Phe	Thr
			180					185					190		

60

Val	Leu	Glu	Leu	Leu	Leu	Ala	Ala	Tyr	Ser	Ser	Val	Phe	Trp	Trp	Lys
		195					200					205			

Gln Leu Tyr Ser Asn Asn Pro Gly Ser Ser Phe Ser Ser Thr Gln Ser  
 210 215 220

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Gln Asp His Ile Gln Gln Val Lys Lys Ser Ser Ser Arg Ser Trp Ile  
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<210> 15

<211> 1369

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<213> Homo sapiens

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<222> (204) .. (956)

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 attctctcag gaaaaaaaaac aagggtcccca cagcaaagaa aaggaatagg atcaagagat 180  
 acgtggctgc tggcagagca agc atg aat tcg atg act tca gca gtt ccg gtg 233  
 Met Asn Ser Met Thr Ser Ala Val Pro Val  
 1 5 10

45

gcc aat tct gtg ttg gtg gtg gca ccc cac aat ggt tat cct gtg acc 281  
 Ala Asn Ser Val Leu Val Val Ala Pro His Asn Gly Tyr Pro Val Thr  
 15 20 25

50

cca gga att atg tct cac gtg ccc ctg tat cca aac agc cag ccg caa 329  
 Pro Gly Ile Met Ser His Val Pro Leu Tyr Pro Asn Ser Gln Pro Gln  
 30 35 40

55

gtc cac cta gtt cct ggg aac cca cct agt ttg gtg tcg aat gtg aat 377  
 Val His Leu Val Pro Gly Asn Pro Pro Ser Leu Val Ser Asn Val Asn  
 45 50 55

60

ggg cag cct gtg cag aaa gct ctg aaa gaa ggc aaa acc ttg ggg gcc 425  
 Gly Gln Pro Val Gln Lys Ala Leu Lys Glu Gly Lys Thr Leu Gly Ala  
 60 65 70



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	Ile Gln Ile Ile Ile Gly Leu Ala His Ile Gly Leu Gly Ser Ile Met	
	75 80 85 90	
10	gcg acg gtt ctc gta ggg gaa tac ctg tct att tca ttc tac gga ggc	521
	Ala Thr Val Leu Val Gly Glu Tyr Leu Ser Ile Ser Phe Tyr Gly Gly	
	95 100 105	
15	ttt ccc ttc tgg gga ggc ttg tgg ttt atc att tca gga tct ctc tcc	569
	Phe Pro Phe Trp Gly Gly Leu Trp Phe Ile Ile Ser Gly Ser Leu Ser	
	110 115 120	
20	gtg gca gca gaa aat cag cca tat tct tat tgc ctg ctg tct ggc agt	617
	Val Ala Ala Glu Asn Gln Pro Tyr Ser Tyr Cys Leu Leu Ser Gly Ser	
	125 130 135	
25	ttg ggc ttg aac atc gtc agt gca atc tgc tct gca gtt gga gtc ata	665
	Leu Gly Leu Asn Ile Val Ser Ala Ile Cys Ser Ala Val Gly Val Ile	
	140 145 150	
30	ctc ttc atc aca gat cta agt att ccc cac cca tat gcc tac ccc gac	713
	Leu Phe Ile Thr Asp Leu Ser Ile Pro His Pro Tyr Ala Tyr Pro Asp	
	155 160 165 170	
35	tat tat cct tac gcc tgg ggt gtg aac cct gga atg gcg att tct ggc	761
	Tyr Tyr Pro Tyr Ala Trp Gly Val Asn Pro Gly Met Ala Ile Ser Gly	
	175 180 185	
40	gtg ctg ctg gtc ttc tgc ctc ctg gag ttt ggc atc gca tgc gca tct	809
	Val Leu Leu Val Phe Cys Leu Leu Glu Phe Gly Ile Ala Cys Ala Ser	
	190 195 200	
45	tcc cac ttt ggc tgc cag ttg gtc tgc tgt caa tca agc aat gtg agt	857
	Ser His Phe Gly Cys Gln Leu Val Cys Cys Gln Ser Ser Asn Val Ser	
	205 210 215	
50	gtc atc tat cca aac atc tat gca gca aac cca gtg atc acc cca gaa	905
	Val Ile Tyr Pro Asn Ile Tyr Ala Ala Asn Pro Val Ile Thr Pro Glu	
	220 225 230	
55	ccg gtg acc tca cca cca agt tat tcc agt gag atc caa gca aat aag	953
	Pro Val Thr Ser Pro Pro Ser Tyr Ser Ser Glu Ile Gln Ala Asn Lys	
	235 240 245 250	
60	taa ggctacagat tctggaagca tctttcactg ggaccaaag aagtcctcct	1006
	ccctttctgg gcttccataa cccaggctcgt tctgttctg acagctgagg aaacgtctct	1066
	cccactgttt gtactctcac cttcattctt caattcagtc taggaaacca tgctgtttct,	1126
	ctatcaagaa gaagacagag attttaaaca gatgttaacc aagagggact ccctagggca	1186
65	catgcatcag cacatatgtg ggcattccagc ctctggggcc ttggcacaca cacattcgtg	1246
	tgctctgctg catgtgagct tgtggggttag aggaacaaat atctagacat tcaatcttca	1306
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 35 40 45  
 30 Asn Pro Pro Ser Leu Val Ser Asn Val Asn Gly Gln Pro Val Gln Lys  
 50 55 60  
 35 Ala Leu Lys Glu Gly Lys Thr Leu Gly Ala Ile Gln Ile Ile Ile Gly  
 65 70 75 80  
 40 Leu Ala His Ile Gly Leu Gly Ser Ile Met Ala Thr Val Leu Val Gly  
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 45 Glu Tyr Leu Ser Ile Ser Phe Tyr Gly Gly Phe Pro Phe Trp Gly Gly  
 100 105 110  
 50 Leu Trp Phe Ile Ile Ser Gly Ser Leu Ser Val Ala Ala Glu Asn Gln  
 115 120 125  
 55 Pro Tyr Ser Tyr Cys Leu Leu Ser Gly Ser Leu Gly Leu Asn Ile Val  
 130 135 140  
 60 Ser Ala Ile Cys Ser Ala Val Gly Val Ile Leu Phe Ile Thr Asp Leu  
 145 150 155 160  
 Ser Ile Pro His Pro Tyr Ala Tyr Pro Asp Tyr Tyr Pro Tyr Ala Trp  
 165 170 175  
 Gly Val Asn Pro Gly Met Ala Ile Ser Gly Val Leu Leu Val Phe Cys  
 180 185 190

5 Leu Leu Glu Phe Gly Ile Ala Cys Ala Ser Ser His Phe Gly Cys Gln  
 195 200 205

10 Leu Val Cys Cys Gln Ser Ser Asn Val Ser Val Ile Tyr Pro Asn Ile  
 210 215 220

15 Tyr Ala Ala Asn Pro Val Ile Thr Pro Glu Pro Val Thr Ser Pro Pro  
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20 Ser Tyr Ser Ser Glu Ile Gln Ala Asn Lys  
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40 cca tca tgg caa gtc ctc agc cca gtc cag ccc tgg cag aca agt gca 96  
 Pro Ser Trp Gln Val Leu Ser Pro Val Gln Pro Trp Gln Thr Ser Ala  
 20 25 30

45 ccc cag aac acg acc cag ccc aag ctc ctg gct cca cac cag cac gag 144  
 Pro Gln Asn Thr Thr Gln Pro Lys Leu Leu Ala Pro His Gln His Glu  
 35 40 45

50 aag tcc cag aag aag agc agc ctt ctt aag gag ctg ggg gcc ttc cac 192  
 Lys Ser Gln Lys Lys Ser Ser Leu Leu Lys Glu Leu Gly Ala Phe His  
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55 atc acc atc gct ctg ctg cac ctg gtc ttt ggg ggc tac ctg gcc tct 240  
 Ile Thr Ile Ala Leu Leu His Leu Val Phe Gly Gly Tyr Leu Ala Ser  
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60 ata gtc aag aac ctt cac ctg gtg gtg ctg aag tct tgg tat cca ttc 288  
 Ile Val Lys Asn Leu His Leu Val Val Leu Lys Ser Trp Tyr Pro Phe  
 85 90 95

	tgg ggg gct gcc tct ttt ctc att tca ggg atc ttg gcg ata aca atg	336
	Trp Gly Ala Ala Ser Phe Leu Ile Ser Gly Ile Leu Ala Ile Thr Met	
	100 105 110	
5	aag acc ttt tct aaa act tac ctg aag atg ttg tgc ctg atg aca aac	384
	Lys Thr Phe Ser Lys Thr Tyr Leu Lys Met Leu Cys Leu Met Thr Asn	
	115 120 125	
10	ctc atc agc ctc ttt tgc gtg ctg tct ggc ctc ttc gtc atc tcc aag	432
	Leu Ile Ser Leu Phe Cys Val Leu Ser Gly Leu Phe Val Ile Ser Lys	
	130 135 140	
15	gat ctc ttt ctg gag agc cca ttt gag tcc ccg atc tgg aga atg tac	480
	Asp Leu Phe Leu Glu Ser Pro Phe Glu Ser Pro Ile Trp Arg Met Tyr	
	145 150 155 160	
20	ccc aac tcc acg gtc cac atc cag agg ctg gag ctg gcc ttg ctc tgc	528
	Pro Asn Ser Thr Val His Ile Gln Arg Leu Glu Leu Ala Leu Leu Cys	
	165 170 175	
25	ttc act gtc cta gag ctc ttc ctg cca gtg ccc aca gct gtc aca gcc	576
	Phe Thr Val Leu Glu Leu Phe Leu Pro Val Pro Thr Ala Val Thr Ala	
	180 185 190	
30	tgg aga ggg gac tgc cca tct gca aag aat gat gat gca tgc ctt gtt	624
	Trp Arg Gly Asp Cys Pro Ser Ala Lys Asn Asp Asp Ala Cys Leu Val	
	195 200 205	
35	ccg aat aca cca ttg cat ctc aaa ggc ctg ccg gtg gag ccc ccg cca	672
	Pro Asn Thr Pro Leu His Leu Lys Gly Leu Pro Val Glu Pro Pro Pro	
	210 215 220	
40	tcc tac cag agt gtg att caa ggc gac gca caa cac aag caa cat cag	720
	Ser Tyr Gln Ser Val Ile Gln Gly Asp Ala Gln His Lys Gln His Gln	
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45	agg tga	726
	Arg	
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60	Pro Gln Asn Thr Thr Gln Pro Lys Leu Leu Ala Pro His Gln His Glu	

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5	Lys Ser Gln Lys Lys Ser Ser Leu Leu Lys Glu Leu Gly Ala Phe His 50 55 60		
10	Ile Thr Ile Ala Leu Leu His Leu Val Phe Gly Gly Tyr Leu Ala Ser 65 70 75 80		
15	Ile Val Lys Asn Leu His Leu Val Val Leu Lys Ser Trp Tyr Pro Phe 85 90 95		
20	Trp Gly Ala Ala Ser Phe Leu Ile Ser Gly Ile Leu Ala Ile Thr Met 100 105 110		
25	Lys Thr Phe Ser Lys Thr Tyr Leu Lys Met Leu Cys Leu Met Thr Asn 115 120 125		
30	Leu Ile Ser Leu Phe Cys Val Leu Ser Gly Leu Phe Val Ile Ser Lys 130 135 140		
35	Asp Leu Phe Leu Glu Ser Pro Phe Glu Ser Pro Ile Trp Arg Met Tyr 145 150 155 160		
40	Pro Asn Ser Thr Val His Ile Gln Arg Leu Glu Leu Ala Leu Leu Cys 165 170 175		
45	Phe Thr Val Leu Glu Leu Phe Leu Pro Val Pro Thr Ala Val Thr Ala 180 185 190		
50	Trp Arg Gly Asp Cys Pro Ser Ala Lys Asn Asp Asp Ala Cys Leu Val 195 200 205		
55	Pro Asn Thr Pro Leu His Leu Lys Gly Leu Pro Val Glu Pro Pro Pro 210 215 220		
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&lt;221&gt; cDNA

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&lt;220&gt;

15 &lt;221&gt; CDS

&lt;222&gt; (148) .. (516)

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25 tctcctcttc tgtaatgagt tggacttgca ggggaaggac ttgtcaaadc ctgaattctt 120

caaggtggta cctcatcagg cagacac atg aag cca gag gag act ggt ggt tct 174  
Met Lys Pro Glu Glu Thr Gly Gly Ser  
1 530 gtt tat cag ccc ttg gat gag tca cgc cat gtt caa cga ggt gta ctg 222  
Val Tyr Gln Pro Leu Asp Glu Ser Arg His Val Gln Arg Gly Val Leu  
10 15 20 2535 caa gcc ctc ggg gcc atc cag atc ctg aat gga ata ctg att cta gct 270  
Gln Ala Leu Gly Ala Ile Gln Ile Leu Asn Gly Ile Leu Ile Leu Ala  
30 35 4040 ctc gga att ttt ctg gtt tgt tta caa cac gtg tcc cac cac ttc agg 318  
Leu Gly Ile Phe Leu Val Cys Leu Gln His Val Ser His His Phe Arg  
45 50 55cat ttc ttc ttc ttc acc ttc tac aca ggc tac cca ctg tgg ggt gct 366  
His Phe Phe Phe Phe Thr Phe Tyr Thr Gly Tyr Pro Leu Trp Gly Ala  
60 65 7045 gtg ttt ttt atc agc tca gga tcc ttg act gtt gcc gca ggg aga aac 414  
Val Phe Phe Ile Ser Ser Gly Ser Leu Thr Val Ala Ala Gly Arg Asn  
75 80 8550 ccc aca cga atg ctg atg caa aac agt ttt ggg ata aac att gcc agt 462  
Pro Thr Arg Met Leu Met Gln Asn Ser Phe Gly Ile Asn Ile Ala Ser  
90 95 100 10555 act aca att gca ttt gtt ggg act gtt ttc ctt tct gtg cat ttg gca 510  
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Phe Asn



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 25 Ile Leu Asn Gly Ile Leu Ile Leu Ala Leu Gly Ile Phe Leu Val Cys  
 35 40 45  
 Leu Gln His Val Ser His His Phe Arg His Phe Phe Phe Phe Thr Phe  
 50 55 60  
 30 Tyr Thr Gly Tyr Pro Leu Trp Gly Ala Val Phe Phe Ile Ser Ser Gly  
 65 70 75 80  
 35 Ser Leu Thr Val Ala Ala Gly Arg Asn Pro Thr Arg Met Leu Met Gln  
 85 90 95  
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5 &lt;220&gt;

&lt;221&gt; CDS

10 &lt;222&gt; (98) .. (778)

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ttccattgtc tgtactgttt ctgctgctct ggaaacc atg caa gga cag gaa cag 115  
Met Gln Gly Gln Glu Gln  
1 5

20 acc acc atg gca gtg gtt cct gga gtt gct gtg cct tca aag aat tct 163  
Thr Thr Met Ala Val Val Pro Gly Val Ala Val Pro Ser Lys Asn Ser  
10 15 20

25 gtt atg aca tca caa atg tgg aat gag aag aaa gag aaa ttc ttg aag 211  
Val Met Thr Ser Gln Met Trp Asn Glu Lys Lys Glu Lys Phe Leu Lys  
25 30 35

30 ggg gaa ccc aaa gtc ctt ggg gtt tta caa gtg atg att gct atc ata 259  
Gly Glu Pro Lys Val Leu Gly Val Leu Gln Val Met Ile Ala Ile Ile  
40 45 50

aac ctc agc tta gga ata ata att ttg aca act tta ttt tct gaa cta 307  
Asn Leu Ser Leu Gly Ile Ile Ile Leu Thr Thr Leu Phe Ser Glu Leu  
55 60 65 70

35 ccc act tca gtg atg tta atg gtc cca att tgg gga tca ata atg ttc 355  
Pro Thr Ser Val Met Leu Met Val Pro Ile Trp Gly Ser Ile Met Phe  
75 80 85

40 att gtc tcc gga tcc ctg tcc att gca gca gga gtg aca cct aca aaa 403  
Ile Val Ser Gly Ser Leu Ser Ile Ala Ala Gly Val Thr Pro Thr Lys  
90 95 100

45 tgc ctg atc gtt gcc agt cta act ctg aac act atc acc tct gtg ttg 451  
Cys Leu Ile Val Ala Ser Leu Thr Leu Asn Thr Ile Thr Ser Val Leu  
105 110 115

50 gct gca act gca agc ata atg ggt gta gtc agt gtg gct gtg ggt tca 499  
Ala Ala Thr Ala Ser Ile Met Gly Val Val Ser Val Ala Val Gly Ser  
120 125 130

cag ttt ccg ttt cgg tat aat tat aca atc acc aag ggt ttg gat gtt 547  
Gln Phe Pro Phe Arg Tyr Asn Tyr Thr Ile Thr Lys Gly Leu Asp Val  
135 140 145 150

55 ttg atg tta att ttc aat atg cta gaa ttc tgc ctt gct gtg tcc gtc 595  
Leu Met Leu Ile Phe Asn Met Leu Glu Phe Cys Leu Ala Val Ser Val  
155 160 165

60 tct gca ttt gga tgt gaa gct tcc tgt tgt aac tcc cgt gag gtt ctt 643  
Ser Ala Phe Gly Cys Glu Ala Ser Cys Cys Asn Ser Arg Glu Val Leu

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5	gta gtg cta cca tca aat cct gtt gag aca gtg atg gca ccc cca atg Val Val Leu Pro Ser Asn Pro Val Glu Thr Val Met Ala Pro Pro Met	691		
	185	190	195	
10	aca ctt caa cca ttg cta cca tca gaa cac caa ggg acc aat gtt cca Thr Leu Gln Pro Leu Leu Pro Ser Glu His Gln Gly Thr Asn Val Pro	739		
	200	205	210	
15	gga aat gtg tac aag aac cac cca gga gaa ata gtc taa ttttgatgtg Gly Asn Val Tyr Lys Asn His Pro Gly Glu Ile Val	788		
	215	220	225	
20	tgtgtgtgtg tatttccta ggatattaac acttcattgc actggctttt gaggtgaata ttagatttac tgtaagtatg taagtcaagc acttattagg tcaacaacac ttcaacatat	848		
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	tatattcatt gtatgtacaa ggggcaatga atttgcaaag atgttttgaa agcaaacaga	968		
25	aaaaaaaaaa aaacaaccaa acaaaagacc tcttagtgaa atgaggtctc tttgcaaaga ctaaaaaact ggagttcaca tttttggggg tgggggggggc ttttgctaaa taagtagatt	1028		
				1088
	tagatgcttt tgatcaagta caaactcata aagtatgtaa gaaattacta atgataggaa	1148		
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	Lys Glu Lys Phe Leu Lys Gly Glu Pro Lys Val Leu Gly Val Leu Gln 35 40 45			
55	Val Met Ile Ala Ile Ile Asn Leu Ser Leu Gly Ile Ile Ile Leu Thr 50 55 60			
60	Thr Leu Phe Ser Glu Leu Pro Thr Ser Val Met Leu Met Val Pro Ile 65 70 75 80			

5 Trp Gly Ser Ile Met Phe Ile Val Ser Gly Ser Leu Ser Ile Ala Ala  
 85 90 95  
 Gly Val Thr Pro Thr Lys Cys Leu Ile Val Ala Ser Leu Thr Leu Asn  
 100 105 110  
 10 Thr Ile Thr Ser Val Leu Ala Ala Thr Ala Ser Ile Met Gly Val Val  
 115 120 125  
 15 Ser Val Ala Val Gly Ser Gln Phe Pro Phe Arg Tyr Asn Tyr Thr Ile  
 130 135 140  
 20 Thr Lys Gly Leu Asp Val Leu Met Leu Ile Phe Asn Met Leu Glu Phe  
 145 150 155 160  
 25 Cys Leu Ala Val Ser Val Ser Ala Phe Gly Cys Glu Ala Ser Cys Cys  
 165 170 175  
 Asn Ser Arg Glu Val Leu Val Val Leu Pro Ser Asn Pro Val Glu Thr  
 180 185 190  
 30 Val Met Ala Pro Pro Met Thr Leu Gln Pro Leu Leu Pro Ser Glu His  
 195 200 205  
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60

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&lt;221&gt; CDS

5 &lt;222&gt; (107) .. (787)

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	tcagatcctt cccattgtct gtactgtttc tgctgccctg gaaacc atg caa gga	115
	Met Gln Gly	
	1	
15	cag gaa cag acc acc atg gca gtg gtt cct gga ggt gct cca cct tca	163
	Gln Glu Gln Thr Thr Met Ala Val Val Pro Gly Gly Ala Pro Pro Ser	
	5 10 15	
20	gag aat tct gtt atg aaa tca caa atg tgg aac gag aac aag gag aaa	211
	Glu Asn Ser Val Met Lys Ser Gln Met Trp Asn Glu Asn Lys Glu Lys	
	20 25 30 35	
25	ttc ttg aag ggg gaa ccc aaa gtc ctt ggg gtt gta caa gtt atg att	259
	Phe Leu Lys Gly Glu Pro Lys Val Leu Gly Val Val Gln Val Met Ile	
	40 45 50	
30	gct ctc ata aac ctc agc ttc gga ata ata att ttg gca aat cta tct	307
	Ala Leu Ile Asn Leu Ser Phe Gly Ile Ile Ile Leu Ala Asn Leu Ser	
	55 60 65	
35	tct gaa cca ctc att tct gtg gtc tta atg gct cca att tgg gga cca	355
	Ser Glu Pro Leu Ile Ser Val Val Leu Met Ala Pro Ile Trp Gly Pro	
	70 75 80	
40	ata atg ttc att gtc tca gga tcc ctg tca att gca gca gga gtg aga	403
	Ile Met Phe Ile Val Ser Gly Ser Leu Ser Ile Ala Ala Gly Val Arg	
	85 90 95	
45	cct aca aaa aag ctg atc atc agc agt cta act ctg aac act atc acc	451
	Pro Thr Lys Lys Leu Ile Ile Ser Ser Leu Thr Leu Asn Thr Ile Thr	
	100 105 110 115	
50	tct gtg ttg gct gca act gca agc ata atg ggt gta gtc agt gtg gct	499
	Ser Val Leu Ala Ala Thr Ala Ser Ile Met Gly Val Val Ser Val Ala	
	120 125 130	
55	gtg ggt tca cag ttt ccg ttt cgg tat aat tat aca atc acc aag ggt	547
	Val Gly Ser Gln Phe Pro Phe Arg Tyr Asn Tyr Thr Ile Thr Lys Gly	
	135 140 145	
60	ttg gat att ttg atg tta att tta aat atg cta gaa ttc tgc att gct	595
	Leu Asp Ile Leu Met Leu Ile Leu Asn Met Leu Glu Phe Cys Ile Ala	
	150 155 160	
60	gtg tcc atc tct gct ttt gga tgt aaa gct tcc tgt tgt aac tcc agc	643
	Val Ser Ile Ser Ala Phe Gly Cys Lys Ala Ser Cys Cys Asn Ser Ser	
	165 170 175	
60	gag gtt ctt gta gtg cta cca tca aat cct gct gtg act gtg atg gca	691

	Glu Val Leu Val Val Leu Pro Ser Asn Pro Ala Val Thr Val Met Ala	
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5	ccc cct gtg acg ctt caa cca ttg cca cca tca gaa cac caa ggg aaa Pro Pro Val Thr Leu Gln Pro Leu Pro Pro Ser Glu His Gln Gly Lys	739
	200 205 210	
10	aat gtt cca gaa aat gta tat aag aac cac tca gaa gaa ata gtc taa Asn Val Pro Glu Asn Val Tyr Lys Asn His Ser Glu Glu Ile Val	787
	215 220 225	
	ttctcttgtg tgtatgtgaa tgtgtgtgtg tgtgtgtgtg tgtgtgtgta tgcatttccc	847
15	tgggaaatta acacttcatt gccctggcct ttgggggggaa tatcagacat gccataactt	907
	tgtaaatcta acatctacta gtacaacaac actttaacat cctccattaa ttgtatgtac	967
	aaggggcaat gaattagcaa agatgttttg aaagcaaaat gaaacaaaca aacaagccag	1027
20	cacacaaaaa aagacctggt ttgtcttttg caaagattaa agaaaggcgt tcacatttct	1087
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25	tatgtatatt atattactaa tgataggaac caatttttat ctctgtgcat attcatcata	1207
	taataacata ctctatactg taattgatat ggtaaaaatt ataataaaga gaagtgactg	1267
	aaatcggaat acacaaacac acacacacac acacatttac atacatagtg tatatctctg	1327
30	tatatacata gtacgtgtat ggtgtgcatg tagagattat agaaggtata catacacata	1387
	tgtgtacata ttacatatga cctaaaaaat cacttataac tgtgggtttgg tgctgtaatc	1447
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	Lys Glu Lys Phe Leu Lys Gly Glu Pro Lys Val Leu Gly Val Val Gln	
60	35 40 45	
	Val Met Ile Ala Leu Ile Asn Leu Ser Phe Gly Ile Ile Ile Leu Ala	



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			Leu Met Ala Pro Ile 80
10	Trp Gly Pro Ile	Met 85	Phe Ile Val Ser Gly 90
			Ser Leu Ser Ile Ala Ala 95
	Gly Val Arg Pro	Thr Lys Lys Leu 100	Ile Ile Ser Ser Leu Thr 110
15	Thr Ile Thr Ser	Val Leu Ala Ala 120	Thr Ala Ser Ile Met Gly Val Val 125
20	Ser Val Ala Val	Gly Ser Gln Phe 135	Pro Phe Arg Tyr Asn Tyr Thr Ile 140
25	Thr Lys Gly Leu	Asp Ile Leu Met Leu 150	Ile Leu Asn Met Leu Glu Phe 160
30	Cys Ile Ala Val	Ser Ile Ser Ala Phe 170	Gly Cys Lys Ala Ser Cys Cys 175
	Asn Ser Ser Glu	Val Leu Val Val 185	Leu Pro Ser Asn Pro Ala Val Thr 190
35	Val Met Ala Pro	Pro Val Thr Leu Gln 200	Pro Leu Pro Pro Ser Glu His 205
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5 &lt;220&gt;

&lt;221&gt; CDS

10 &lt;222&gt; (36) .. (713)

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1 5

20 acc acc atg gca gtg gtt cct gga ggt gct cca cct tca gag aat tct 101  
Thr Thr Met Ala Val Val Pro Gly Gly Ala Pro Pro Ser Glu Asn Ser  
10 15 20

25 gtt ata aaa tca caa atg tgg aac aag aac aaa gag aaa ttc ttg aag 149  
Val Ile Lys Ser Gln Met Trp Asn Lys Asn Lys Glu Lys Phe Leu Lys  
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Gly Glu Pro Lys Val Leu Gly Ala Ile Gln Val Met Ile Ala Phe Ile  
40 45 50

30 aac ttc agc tta gga ata ata att ata tta aat aga gtt tct gaa cga 245  
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55 60 65 70

35 ttc atg tca gtg ctc tta ctg gcc cca ttt tgg gga tca ata atg ttc 293  
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       atcttctatt cattgtatgt acaagaagaa tttaattggc aaaaaaaatt ttaatgtaaa      903

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	Phe His Gln Trp Gln Asp Ser Leu Lys Lys His Leu Lys Ala Glu Ile	
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	Thr Lys Ile Leu Val Asp Ser Ser Leu Thr Leu Asn Ile Leu Ser Val	
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	Ser Phe Ala Phe Met Gly Ile Ile Ile Ser Val Ser Leu Ala Gly	
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	Thr Glu Tyr His Tyr Tyr Gln Phe Leu Asp Arg Asn Glu Cys Phe Ala	
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	Ala Lys Ser Val Leu Ala Gly Val Phe Ser Leu Met Leu Ile Ser Thr	
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	Met Leu Glu Leu Gly Leu Ala Val Leu Thr Ala Met Leu Trp Trp Lys	
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5	cag agt cac tct aac atc cct ggg aat gtt atg ttc ctg cca cat agc	795
	Gln Ser His Ser Asn Ile Pro Gly Asn Val Met Phe Leu Pro His Ser	
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	Tyr Glu Glu Gln Leu Val Cys	
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40	His	Tyr	Tyr	Gln	Phe	Leu	Asp	Arg	Asn	Glu	Cys	Phe	Ala	Ala	Lys	Ser
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15	tgc aag cag agc aag gag ctt agt cta att gaa cat gac tac tac caa Cys Lys Gln Ser Lys Glu Leu Ser Leu Ile Glu His Asp Tyr Tyr Gln	655		
20	cct ttc tac aac tca gac agg agt gaa tgt gcc gtc acc aag tct att Pro Phe Tyr Asn Ser Asp Arg Ser Glu Cys Ala Val Thr Lys Ser Ile	703		
25	ctg act gga gcc ctt tca gtg atg ctg atc atc agt gtg ttg gag ctt Leu Thr Gly Ala Leu Ser Val Met Leu Ile Ile Ser Val Leu Glu Leu	751		
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5	Val	Leu	Leu	Lys	Ser	Gly	Tyr	Pro	Phe	Ile	Gly	Ala	Leu	Phe	Phe	Ile	
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25 agc ctg aag aaa cat cta aag gct gag atc aaa gtg atg gcg gca atc 262  
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60 gct ctg act gga gtc ttt tca ctg atg cta atc agc agt gtg ttg gag 694  
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			195					200					205				
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35 ctg ctg att gga gtg cct agt gaa gcc aca ctt ctt gga acc atc cag 260  
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 Ala Ser Tyr Phe Asn Pro Glu Val Ser Thr Thr Leu Ile Ser Gly Tyr  
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45 ctg ttt att gga tcc ctc tgt ttt gcc att gct gga att ctc tcc att 404  
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50 atc tct gaa aaa atc tca acc aaa ccc ttt gca ctg agc agc ctg gcc 452  
 Ile Ser Glu Lys Ile Ser Thr Lys Pro Phe Ala Leu Ser Ser Leu Ala  
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 Ser Asn Val Ala Ser Ser Val Val Ala Val Ile Gly Leu Phe Leu Phe  
 120 125 130

55 acc tat tgt ctg ata gcc ctg ggg agt gct ttc cca cac tgt aac tca 548  
 Thr Tyr Cys Leu Ile Ala Leu Gly Ser Ala Phe Pro His Cys Asn Ser  
 135 140 145

60 gaa aag aaa ttc ctg tcc tta ttg tct tac ttg aaa tcc cac cat tgg 596  
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60	Ile Leu Val Ser Ala Ser Tyr Phe Asn Pro Glu Val Ser Thr Thr Leu 65 70 75 80			
	Ile Ser Gly Tyr Leu Phe Ile Gly Ser Leu Cys Phe Ala Ile Ala Gly			

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5	Ile Leu Ser Ile Ile Ser Glu Lys Ile Ser Thr Lys Pro Phe Ala Leu 100 105 110		
10	Ser Ser Leu Ala Ser Asn Val Ala Ser Ser Val Val Ala Val Ile Gly 115 120 125		
15	Leu Phe Leu Phe Thr Tyr Cys Leu Ile Ala Leu Gly Ser Ala Phe Pro 130 135 140		
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25	Ser His His Trp Lys Asn Glu Asp Lys Asn Cys Tyr Leu Ala Tyr Val 165 170 175		
30	Gly Ala Met Ser Ala Leu Gly Met Met Leu Leu Phe Thr Val Leu Glu 180 185 190		
35	Val Phe Leu Ala Gly Tyr Ser Ser Ile Phe Trp Trp Lys Gln Val Tyr 195 200 205		
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	Thr Val Ser Met Asn Thr Val Thr Ser Pro Gly Pro Met Ala Asn Ser	
	15 20 25	
20	gta tat gtg gtg gca ccg ccc aac agt tat cct gtg gtc cca gga acc	146
	Val Tyr Val Val Ala Pro Pro Asn Ser Tyr Pro Val Val Pro Gly Thr	
	30 35 40 45	
25	gtg cct cag atg cct att tat ccc agc aat cag cct caa gtc cat gtg	194
	Val Pro Gln Met Pro Ile Tyr Pro Ser Asn Gln Pro Gln Val His Val	
	50 55 60	
30	att tct ggt cat ctg cct ggt ttg gtg cca gct atg acc gaa cca cct	242
	Ile Ser Gly His Leu Pro Gly Leu Val Pro Ala Met Thr Glu Pro Pro	
	65 70 75	
35	gcc cag aga gtc ttg aaa aag gga caa gtc cta ggg gcc atc cag atc	290
	Ala Gln Arg Val Leu Lys Lys Gly Gln Val Leu Gly Ala Ile Gln Ile	
	80 85 90	
40	ctg atc ggc ctg gtg cac atc ggc ctg ggc tcc atc atg atc acc aac	338
	Leu Ile Gly Leu Val His Ile Gly Leu Gly Ser Ile Met Ile Thr Asn	
	95 100 105	
45	ctc ttc agc cac tat aca cct gtc tcc ctc tat gga ggt ttc ccc ttc	386
	Leu Phe Ser His Tyr Thr Pro Val Ser Leu Tyr Gly Gly Phe Pro Phe	
	110 115 120 125	
50	tgg gga ggc atc tgg ttt atc att tca gga tct ctc tca gtg gcg gca	434
	Trp Gly Gly Ile Trp Phe Ile Ile Ser Gly Ser Leu Ser Val Ala Ala	
	130 135 140	
55	gaa act cag ccc aat tca cct tgc ctg ctg aat ggc agt gtg ggc ttg	482
	Glu Thr Gln Pro Asn Ser Pro Cys Leu Leu Asn Gly Ser Val Gly Leu	
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	Asn Ile Phe Ser Ala Ile Cys Ser Ala Val Gly Ile Met Leu Phe Ile	
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	Thr Asp Ile Ser Ile Ser Ser Gly Tyr Ile Tyr Pro Ser Tyr Tyr Pro	
	175 180 185	
70	tac cag gag aac ttg ggt gtg aga aca ggc gtg gct att tct agt gtg	626
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	Leu Leu Ile Phe Cys Leu Leu Glu Leu Ser Ile Ala Ser Val Ser Ser	

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10	gtc att cca aat gtc tat gca gca aac cca gtg gtc atc cca gaa cca			770
	Val Ile Pro Asn Val Tyr Ala Ala Asn Pro Val Val Ile Pro Glu Pro			
	240	245	250	
15	cca aac cca ata cca agt tat tcc gaa gta gtt caa gac tcc aga taa			818
	Pro Asn Pro Ile Pro Ser Tyr Ser Glu Val Val Gln Asp Ser Arg			
	255	260	265	
20	gtgaacctga agattctaga gaccaagtga catcctctcc tacctagact cctataaacc			878
	aagttcttcc tttcctgacg aagggtaaat atctttcttg tggcctaaat tatagactct			938
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45	Val Ala Pro Pro Asn Ser Tyr Pro Val Val Pro Gly Thr Val Pro Gln			
	35 40 45			
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	50 55 60			
55	His Leu Pro Gly Leu Val Pro Ala Met Thr Glu Pro Pro Ala Gln Arg			
	65 70 75 80			
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	85 90 95			
60	Leu Val His Ile Gly Leu Gly Ser Ile Met Ile Thr Asn Leu Phe Ser			
	100 105 110			



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 115 120 125  
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 10 Pro Asn Ser Pro Cys Leu Leu Asn Gly Ser Val Gly Leu Asn Ile Phe  
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 15 Ser Ala Ile Cys Ser Ala Val Gly Ile Met Leu Phe Ile Thr Asp Ile  
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 20 Ser Ile Ser Ser Gly Tyr Ile Tyr Pro Ser Tyr Tyr Pro Tyr Gln Glu  
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	Val Thr Gly Glu Val Ser Arg Trp Gln Asn Leu Gly Pro Ala Gln Pro	
	15 20 25	
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	Ala Gln Lys Val Ala Gln Pro Gln Asn Leu Val Pro Asp Gly His Leu	
	30 35 40	
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	Glu Lys Ala Leu Glu Gly Ser Asp Leu Leu Gln Lys Leu Gly Gly Phe	
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	Ser Thr Val Lys Asn Leu His Leu Val Val Leu Lys Cys Trp Tyr Pro	
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	Leu Trp Gly Thr Val Ser Phe Leu Val Ala Gly Met Ala Ala Met Thr	
	95 100 105	
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	110 115 120	
45	aac gtt atc agc ttg ttc tgc gca ctg gcc ggc ttc ttt gtc att gcc	494
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	Cys Phe Thr Phe Leu Glu Ile Phe Leu Ser Gly Ser Thr Ala Ile Thr	
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	Pro	Pro	Ser	Tyr	Lys	Asp	Val	Ala	Gln	Gly	His	Ser	Ser	Ser	Asp	Thr	
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	Val	Ser	Phe	Leu	Val	Ala	Gly	Met	Ala	Ala	Met	Thr	Thr	Val	Thr	Phe
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5	Pro	Lys	Thr	Ser	Leu	Lys	Val	Leu	Cys	Val	Ile	Ala	Asn	Val	Ile	Ser
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15     <302>  Structure of the gene encoding the human B lymphocyte
      differentiation antigen CD20 (B1)
      <303>  J Immunol

20     <304>  142
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      <306>  2560-2568

25     <307>  1989-__-__
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30     <300>
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35     <302>  Isolation and structure of a cDNA encoding the B1 (CD20) cell-
      surface antigen of human B lymphocytes
      <303>  Proc Natl Acad Sci USA
      <304>  85
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                   1             5             10

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	30				35				40								
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	45				50				55				60				
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	65				70				75								
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<302> The gene and cDNA for the human high affinity immunoglobulin E  
 15 receptor beta chain and expression of the complete human receptor

<303> J Biol Cham

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 30 <302> Cloning of the cDNA for a hematopoietic cell-specific protein  
 related to CD20 and the beta subunit of the high-affinity IgE receptor:  
 evidence for a family of proteins with four membrane-spanning regions  
 <303> Proc Natl Acad Sci USA  
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<301> Tedder, TF, Klejman, G, Disteché, CM, Adler, DA, Schlossman, SF,  
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<302> Cloning of complementary DNA encoding a new mouse B lymphocyte  
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<303> J Immunol

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55	<304> 264		

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